

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:59:48 ; Search time 20 Seconds
(without alignments)
1723.788 Million cell updates/sec

Title: US-10-081-280-6

Perfect score: 2323

Sequence: 1 MEQPRGCAAAVALLLVLL.....ERMGLGCVEDLRSLRQRP 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCRTUS COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2323	100.0	417	2	US-08-815-469-4
2	2323	100.0	417	2	US-09-153-927-2
3	2323	100.0	417	2	US-09-565-918-5
4	2323	100.0	417	2	US-08-928-069-10
5	2323	100.0	417	2	US-08-828-683A-6
6	2323	100.0	417	2	US-09-557-908-4
7	2323	100.0	417	2	US-09-874-138-5
8	2323	100.0	417	2	US-09-333-966-4
9	2323	100.0	417	2	US-09-565-009B-5
10	2323	100.0	417	2	US-10-175-902-5
11	2323	100.0	417	2	US-09-314-889-4
12	2323	100.0	446	2	US-09-949-016-7652
13	2323	100.0	833	2	US-09-013-895A-5
14	2323	100.0	833	2	US-09-448-868-5
15	2323	100.0	833	2	US-10-226-296-5
16	2267	97.6	428	2	US-08-815-469-2
17	2267	97.6	428	2	US-09-557-908-2
18	2267	97.6	428	2	US-09-333-966-2
19	2267	97.6	428	2	US-09-314-889-2
20	1051	45.2	181	2	US-08-928-069-1
21	1051	45.2	181	2	US-08-828-683A-1
22	387.5	16.7	471	2	US-09-513-007-2
23	387.5	16.7	471	2	US-09-970-532-2
24	376	16.2	455	1	US-08-050-319B-25
25	376	16.2	455	1	US-08-465-982-25
26	376	16.2	455	2	US-08-406-824A-4
27	374.5	16.1	909	2	US-09-013-895A-4

28	374.5	16.1	909	2	US-09-448-868-4	Sequence 4, Appli
29	374.5	16.1	909	2	US-10-226-296-4	Sequence 4, Appli
30	374	16.1	455	1	US-08-321-668-2	Sequence 2, Appli
31	374	16.1	455	1	US-08-837-941-2	Sequence 2, Appli
32	374	16.1	455	1	US-08-126-016-2	Sequence 5, Appli
33	374	16.1	455	2	US-08-815-469-5	Sequence 5, Appli
34	374	16.1	455	2	US-09-006-353A-3	Sequence 5, Appli
35	374	16.1	455	2	US-09-527-236A-5	Sequence 5, Appli
36	374	16.1	455	2	US-08-054-970-2	Sequence 4, Appli
37	374	16.1	455	2	US-09-565-918-4	Sequence 4, Appli
38	374	16.1	455	2	US-09-573-986-3	Sequence 3, Appli
39	374	16.1	455	2	US-09-027-287-3	Sequence 3, Appli
40	374	16.1	455	2	US-09-252-656B-3	Sequence 3, Appli
41	374	16.1	455	2	US-09-523-323-3	Sequence 3, Appli
42	374	16.1	455	2	US-09-756-854-5	Sequence 5, Appli
43	374	16.1	455	2	US-09-557-908-5	Sequence 5, Appli
44	374	16.1	455	2	US-09-874-138-3	Sequence 3, Appli
45	374	16.1	455	2	US-09-333-966-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-815-469-4
; Sequence 4, Application US/08815469
; Patent No. 6153402
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillion, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 6153402 Yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-815-469-4

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORPRGCAAAVAAALLVLLGARAQGGTRSPRCDACGDFHKKIGLFCRCRCPAGHYLKAP 60
DB 1 MEORPRGCAAAVAAALLVLLGARAQGGTRSPRCDACGDFHKKIGLFCRCRCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAQCAQDEQASQVALENCASAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAQCAQDEQASQVALENCASAVADTRCGCKPG 120
QY 121 WFVEQVQSCVSSPPFYCQPCDCLGALHRRHTRLLCSRDDTCGTCLPGFVEHGDGCVSCP 180
DB 121 WFVEQVQSCVSSPPFYCQPCDCLGALHRRHTRLLCSRDDTCGTCLPGFVEHGDGCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCHWPKPLVTADG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCHWPKPLVTADG 240
QY 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTPGYPETQALCPQVTWSW 300
DB 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTPGYPETQALCPQVTWSW 300
QY 301 DQPSRALGPAAPTLSPEPAGSPAMMLOQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
DB 301 DQPSRALGPAAPTLSPEPAGSPAMMLOQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
QY 361 IEAVEVEIGFRDQOQYEMLRWQOQPGAGLVAVYALERMGLDGCVEDLRSRQGP 417
DB 361 IEAVEVEIGFRDQOQYEMLRWQOQPGAGLVAVYALERMGLDGCVEDLRSRQGP 417

RESULT 2

US-153-927-2
; Sequence 2, Application US/09153927A
; Patent No. 6297022
; GENERAL INFORMATION:
; APPLICANT: McDonnell, Peter C.
; APPLICANT: Young, Peter R.
; TITLE OF INVENTION: A Method of Identifying Agonists and Antagonists for Tumor Necrosis Related Receptors TR1, TR3
; TITLE OF INVENTION: and TR5
; FILE REFERENCE: GH50031
; CURRENT APPLICATION NUMBER: US/09/153,927A
; CURRENT FILING DATE: 1998-09-16
; EARLIER APPLICATION NUMBER: 60/061,334
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Human
US-09-153-927-2

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORPRGCAAAVAAALLVLLGARAQGGTRSPRCDACGDFHKKIGLFCRCRCPAGHYLKAP 60
DB 1 MEORPRGCAAAVAAALLVLLGARAQGGTRSPRCDACGDFHKKIGLFCRCRCPAGHYLKAP 60
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DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAQCAQDEQASQVALENCASAVADTRCGCKPG 120
QY 121 WFVEQVQSCVSSPPFYCQPCDCLGALHRRHTRLLCSRDDTCGTCLPGFVEHGDGCVSCP 180

DB 121 WFVEQVQSCVSSPPFYCQPCDCLGALHRRHTRLLCSRDDTCGTCLPGFVEHGDGCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCHWPKPLVTADG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCHWPKPLVTADG 240
QY 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTPGYPETQALCPQVTWSW 300
DB 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTPGYPETQALCPQVTWSW 300
QY 301 DQPSRALGPAAPTLSPEPAGSPAMMLOQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
DB 301 DQPSRALGPAAPTLSPEPAGSPAMMLOQPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
QY 361 IEAVEVEIGFRDQOQYEMLRWQOQPGAGLVAVYALERMGLDGCVEDLRSRQGP 417
DB 361 IEAVEVEIGFRDQOQYEMLRWQOQPGAGLVAVYALERMGLDGCVEDLRSRQGP 417

RESULT 3

US-09-565-918-5
; Sequence 5, Application US/09565918
; Patent No. 6433147
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4
; FILE REFERENCE: 1488.1300005
; CURRENT APPLICATION NUMBER: US/09/565,918
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: US 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: US 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: US 60/035,722
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-918-5

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORPRGCAAAVAAALLVLLGARAQGGTRSPRCDACGDFHKKIGLFCRCRCPAGHYLKAP 60
DB 1 MEORPRGCAAAVAAALLVLLGARAQGGTRSPRCDACGDFHKKIGLFCRCRCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAQCAQDEQASQVALENCASAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAQCAQDEQASQVALENCASAVADTRCGCKPG 120
QY 121 WFVEQVQSCVSSPPFYCQPCDCLGALHRRHTRLLCSRDDTCGTCLPGFVEHGDGCVSCP 180
DB 121 WFVEQVQSCVSSPPFYCQPCDCLGALHRRHTRLLCSRDDTCGTCLPGFVEHGDGCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCHWPKPLVTADG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCHWPKPLVTADG 240
QY 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTPGYPETQALCPQVTWSW 300
DB 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTPGYPETQALCPQVTWSW 300

QY 301 DOLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAE 360
Db 301 DOLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQRP 417

RESULT 4

US-08-928-069-10
; Sequence 10, Application US/08928069
; Patent No. 6462176
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,069
; FILING DATE: 11-Sep-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/026943
; FILING DATE: 09/23/1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1052R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-928-069-10

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MEORPRGCAVAAALLLVLLGARAQGGTSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCNSAVADTRCCCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCNSAVADTRCCCKPG 120
QY 121 WFVECVQSCVSSSPFYCQPCLDGALHHRHLLCSRRTDCGTCLPGFVEHGDGCVSCP 180
Db 121 WFVECVQSCVSSSPFYCQPCLDGALHHRHLLCSRRTDCGTCLPGFVEHGDGCVSCP 180
QY 181 TSTLGSCLPCCAAVCCWRQMFVQVLLAGLVVPLLIGATLTYTTRHCWHPKPLVTADG 240
Db 181 TSTLGSCLPCCAAVCCWRQMFVQVLLAGLVVPLLIGATLTYTTRHCWHPKPLVTADG 240
QY 241 MEALTPPPATHLSPLDSAHLLAPDSSEKICTVQLVGNWSWTPGYPETQALCPQVTSW 300
Db 241 MEALTPPPATHLSPLDSAHLLAPDSSEKICTVQLVGNWSWTPGYPETQALCPQVTSW 300

QY 301 DOLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAE 360
Db 301 DOLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQRP 417

RESULT 5

US-08-828-683A-6
; Sequence 6, Application US/08828683A
; Patent No. 6469144
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-828-683A-6

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEORPRGCAVAAALLLVLLGARAQGGTSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEORPRGCAVAAALLLVLLGARAQGGTSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCNSAVADTRCCCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCNSAVADTRCCCKPG 120
QY 121 WFVECVQSCVSSSPFYCQPCLDGALHHRHLLCSRRTDCGTCLPGFVEHGDGCVSCP 180
Db 121 WFVECVQSCVSSSPFYCQPCLDGALHHRHLLCSRRTDCGTCLPGFVEHGDGCVSCP 180
QY 181 TSTLGSCLPCCAAVCCWRQMFVQVLLAGLVVPLLIGATLTYTTRHCWHPKPLVTADG 240
Db 181 TSTLGSCLPCCAAVCCWRQMFVQVLLAGLVVPLLIGATLTYTTRHCWHPKPLVTADG 240

Db 361 IEAVEIGRFRDQOQYEMLKRWQOQAGVAVYAAALERMGLDGCVEDLRSRLQRP 417

RESULT 8

US-09-333-966-4
; Sequence 4, Application US/09333966
; Patent No. 6759513
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/333,966
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE:
; APPLICATION NUMBER: No. 6759513 Yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-333-966-4

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPRGCAVAAALLLVLLGARAQGGTSPRCDGADFHKKI GLFCRCGPAGHYLKAP 60
Db 1 MEQRPRGCAVAAALLLVLLGARAQGGTSPRCDGADFHKKI GLFCRCGPAGHYLKAP 60
QY 61 CTPECGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCNSAVADTRCGCKPG 120
Db 61 CTPECGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVEQVQSCVSSSPFYCPCLDCGALHRRHRLTLLCSRRDTCGTCLPGFVEHGDGCVSCP 180
Db 121 WFVEQVQSCVSSSPFYCPCLDCGALHRRHRLTLLCSRRDTCGTCLPGFVEHGDGCVSCP 180

QY 181 TSTLASCPRCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHCHPHKPLVTADAG 240
Db 181 TSTLASCPRCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHCHPHKPLVTADAG 240
QY 241 MEALTPPPATHLSPLDSAHTLAPDSSSEKI CTQVLVGNSTPGYPETQALCPQVTWSW 300
Db 241 MEALTPPPATHLSPLDSAHTLAPDSSSEKI CTQVLVGNSTPGYPETQALCPQVTWSW 300
QY 301 DQLPSRALGPAAPLTLSPSPAGSPAMMLQPGPOLYDVNDVAPARWKEFVRTLGLREAE 360
Db 301 DQLPSRALGPAAPLTLSPSPAGSPAMMLQPGPOLYDVNDVAPARWKEFVRTLGLREAE 360
QY 361 IEAVEIGRFRDQOQYEMLKRWQOQAGVAVYAAALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEIGRFRDQOQYEMLKRWQOQAGVAVYAAALERMGLDGCVEDLRSRLQRP 417

RESULT 9

US-09-565-009B-5
; Sequence 5, Application US/09565009B
; Patent No. 6872568
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Death Domain Containing Receptor 5
; FILE REFERENCE: 1488.1310006
; CURRENT APPLICATION NUMBER: US/09/565,009B
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/148,939
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/133,238
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/132,498
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 09/042,583
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: 60/054,021
; PRIOR FILING DATE: 1997-07-29
; PRIOR APPLICATION NUMBER: 60/040,846
; PRIOR FILING DATE: 1997-03-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 417
; TYPE: PRI
; ORGANISM: Homo sapiens
US-09-565-009B-5

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPRGCAVAAALLLVLLGARAQGGTSPRCDGADFHKKI GLFCRCGPAGHYLKAP 60
Db 1 MEQRPRGCAVAAALLLVLLGARAQGGTSPRCDGADFHKKI GLFCRCGPAGHYLKAP 60
QY 61 CTPECGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCNSAVADTRCGCKPG 120
Db 61 CTPECGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVEQVQSCVSSSPFYCPCLDCGALHRRHRLTLLCSRRDTCGTCLPGFVEHGDGCVSCP 180
Db 121 WFVEQVQSCVSSSPFYCPCLDCGALHRRHRLTLLCSRRDTCGTCLPGFVEHGDGCVSCP 180
QY 181 TSTLASCPRCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHCHPHKPLVTADAG 240
Db 181 TSTLASCPRCAAVCGWRQMFVQVLLAGLVPLLLGATLTYYRHCHPHKPLVTADAG 240
QY 241 MEALTPPPATHLSPLDSAHTLAPDSSSEKI CTQVLVGNSTPGYPETQALCPQVTWSW 300
Db 241 MEALTPPPATHLSPLDSAHTLAPDSSSEKI CTQVLVGNSTPGYPETQALCPQVTWSW 300

QY 301 DQLPSRALGPAAPTLSPEPAGSPAMMLQPGQLYDVMQVAVPARRWKEFVRTLGLREAE 360
Db 301 DQLPSRALGPAAPTLSPEPAGSPAMMLQPGQLYDVMQVAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGFRDQOQYEMLRWQOQAGLQAGVAVPARRWKEFVRTLGLREAE 417
Db 361 IEAVEVEIGFRDQOQYEMLRWQOQAGLQAGVAVPARRWKEFVRTLGLREAE 417

RESULT 10

US-10-175-902-5
; Sequence 5, Application US/10175902
; Patent No. 6902910
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4
; FILE REFERENCE: 1488.1300005
; CURRENT APPLICATION NUMBER: US/10/175,902
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 09/565,918
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: US 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: US 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: US 60/035,722
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-175-902-5

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEQPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVEQVQSVSSPPFYCQPCLDGALHRRHTRLLCSRRDTCGTCLPGFYHGDGCVSCP 180
Db 121 WFVEQVQSVSSPPFYCQPCLDGALHRRHTRLLCSRRDTCGTCLPGFYHGDGCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCWHPKPLVTADAG 240
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCWHPKPLVTADAG 240
QY 241 MEALTTPPATLSPDLSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQALCPQVTWSW 300
Db 241 MEALTTPPATLSPDLSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQALCPQVTWSW 300
QY 301 DQLPSRALGPAAPTLSPEPAGSPAMMLQPGQLYDVMQVAVPARRWKEFVRTLGLREAE 360
Db 301 DQLPSRALGPAAPTLSPEPAGSPAMMLQPGQLYDVMQVAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGFRDQOQYEMLRWQOQAGLQAGVAVPARRWKEFVRTLGLREAE 417
Db 361 IEAVEVEIGFRDQOQYEMLRWQOQAGLQAGVAVPARRWKEFVRTLGLREAE 417

RESULT 11

US-09-314-889-4
; Sequence 4, Application US/09314889
; Patent No. 6951735
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/314,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/815,469
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-314-889-4

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 3.5e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEQPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVEQVQSVSSPPFYCQPCLDGALHRRHTRLLCSRRDTCGTCLPGFYHGDGCVSCP 180
Db 121 WFVEQVQSVSSPPFYCQPCLDGALHRRHTRLLCSRRDTCGTCLPGFYHGDGCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCWHPKPLVTADAG 240
Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCWHPKPLVTADAG 240

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Qy 241 MEALTTPPPATHSLPDSAHITLLAPPDSSSEKICTVQLVGNSWTPGYPETQBALCPQVTWSW 300
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Db 241 MEALTTPPPATHSLPDSAHITLLAPPDSSSEKICTVQLVGNSWTPGYPETQBALCPQVTWSW 300
    |||||
Qy 301 DQLPSPRALGPAAAPTLSPEPSAGSPAMMLQPGLPOLYDVMDAVPARRWKFEFVRTTLGLREAE 360
    |||||
Db 301 DQLPSPRALGPAAAPTLSPEPSAGSPAMMLQPGLPOLYDVMDAVPARRWKFEFVRTTLGLREAE 360
    |||||
Qy 361 IEAVEVEIGRFRDOQOYEMLKEWRQQOPAGLGANVAALERMGLDCGVEDLRSLRQGP 417
    |||||
Db 361 IEAVEVEIGRFRDOQOYEMLKEWRQQOPAGLGANVAALERMGLDCGVEDLRSLRQGP 417
    |||||

RESULT 12
US-09-949-016-7652
; Sequence 7652, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7652
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-7652

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US-09-013-895A-5
; Sequence 5, Application US/09013895A
; Patent No. 6342363
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
; TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
; TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013.895A
; FILING DATE: 27-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1300002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 833 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-013-895A-5

RESULT 13

QY 361 IEAVEVEIGRFRDQOYEMLKRWKROQOPAGLGAVYAALERMGLDGCVEDLSRLQGRP 417
Db 361 IEAVEVEIGRFRDQOYEMLKRWKROQOPAGLGAVYAALERMGLDGCVEDLSRLQGRP 417

RESULT 14

US-09-448-868-5
; Sequence 5, Application US/09448868
; Patent No. 6461823
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
; Receptor 4), Member of the TNF-Receptor
; TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/448,868
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/013,895
; FILING DATE: 27-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1300004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 833 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-448-868-5

Query Match 100.0%; Score 2323; DB 2; Length 833;
Best Local Similarity 100.0%; Pred. No. 8.4e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MEORPRGCAVAAALLLVLLGARAQGGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAACACDEQASQVALENCNSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAACACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVEQCVSQVSSPFYQPCPLDCGALHRRHTRLLCSRRDTCCTCLPGFVEHGDGCVSCP 180
Db 121 WFVEQCVSQVSSPFYQPCPLDCGALHRRHTRLLCSRRDTCCTCLPGFVEHGDGCVSCP 180
QY 181 TSTLGSCPERRCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPKPLVTADEAG 240

Db 181 TSTLGSCPERRCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPKPLVTADEAG 240
QY 241 MEALTTPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTWPGYPTQALCPQVTWSW 300
Db 241 MEALTTPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTWPGYPTQALCPQVTWSW 300
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Db 301 DQLPSRALGPAAAPTILSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKSFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQOYEMLKRWKROQOPAGLGAVYAALERMGLDGCVEDLSRLQGRP 417
Db 361 IEAVEVEIGRFRDQOYEMLKRWKROQOPAGLGAVYAALERMGLDGCVEDLSRLQGRP 417

RESULT 15

US-10-226-296-5
; Sequence 5, Application US/10226296
; Patent No. 6943020
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death
; Receptor 4), Member of the TNF-Receptor
; TITLE OF INVENTION: Superfamily and Binding to Trail (AP02-L)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/226,296
; FILING DATE: 23-AUG-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/448,868
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/013,895
; FILING DATE: 27-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1300004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 833 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-226-296-5

Query Match 100.0%; Score 2323; DB 2; Length 833;
Best Local Similarity 100.0%; Pred. No. 8.4e-193;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEORPRGCAVAAALLLVLLGARAQGGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60

Db	1	MEQPRGCAVAAALLLVILGARAOGTRSPRCDGAGDFHKKIKIGLFCRCRCPAGHYLKAP	60
Qy	61	CTEPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCNSAVADTRCGCKPG	120
Db	61	CTEPCGNSTCLVCPQDTFLAWENHNHNSCARQACDEQASQVALENCNSAVADTRCGCKPG	120
Qy	121	WFVEQVSCVSSSPFYCOPCLDCGALHRRHRLLCRRDTCGTCLPGFYEHDGCVSCP	180
Db	121	WFVEQVSCVSSSPFYCOPCLDCGALHRRHRLLCRRDTCGTCLPGFYEHDGCVSCP	180
Qy	181	TSTLGSCEPCERCAAVCGWRQWVQVLLAGLVVPLLIGATLTYTYRHCWPHKPLVTADAG	240
Db	181	TSTLGSCEPCERCAAVCGWRQWVQVLLAGLVVPLLIGATLTYTYRHCWPHKPLVTADAG	240
Qy	241	MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVQLVGNSTPGYPETOALCPQVTSW	300
Db	241	MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVQLVGNSTPGYPETOALCPQVTSW	300
Qy	301	DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE	360
Db	301	DQLPSRALGPAAAPTLSPESPAGSPAMMLQPGPQLYDVMDAVPARRWKEFVRTLGLREAE	360
Qy	361	IEAVEVEIGFRDQOQYEMLKRWRQOQAGLGAVYAALERMGLDGCVEDLRSRLQGP	417
Db	361	IEAVEVEIGFRDQOQYEMLKRWRQOQAGLGAVYAALERMGLDGCVEDLRSRLQGP	417

Search completed: March 20, 2006, 08:00:16
 Job time : 21 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:59:25 ; Search time 27 Seconds
(without alignments)
1486.014 Million cell updates/sec

Title: US-10-081-280-6

Perfect score: 2323

Sequence: 1 MEQRPRGCAVAALLLVLL.....ERMGLDGCVEDLRSRLQRP 417

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	415	17.9	461	JC4302	tumor necrosis fac
2	404.5	17.4	454	1 GQWST1	tumor necrosis fac
3	394.5	17.0	461	1 GQRTT1	tumor necrosis fac
4	374	16.1	455	1 GQRTU1	tumor necrosis fac
5	199.5	8.6	335	2 A40036	apoptosis-mediatin
6	196	8.4	337	2 A46484	apoptosis-mediatin
7	175	7.5	324	2 JC2395	Fas antigen precu
8	168	7.2	314	2 I37383	FAS soluble protei
9	166	7.1	435	2 I54182	tumor necrosis fac
10	163.5	7.0	1548	2 S34583	serine proteinase
11	162.5	7.0	349	2 D36858	gene G4R protein -
12	159.5	6.9	348	2 T28623	hypothetical prote
13	158	6.8	425	1 A26431	nerve growth facto
14	158	6.8	1574	2 T13954	MEGF6 protein - ra
15	155.5	6.7	427	1 GQHUN	nerve growth facto
16	154.5	6.7	349	2 D72175	G2R protein - vari
17	153.5	6.6	272	2 I48700	gene ox40 protein
18	153.5	6.6	651	2 JC7705	death receptor-6 -
19	153.5	6.6	915	1 A48225	subtilisin-like pr
20	149.5	6.4	3707	2 S18252	heparan sulfate pr
21	148	6.4	2823	2 F87908	protein T22A3.8 [i
22	148	6.4	2823	2 T23064	hypothetical prote
23	148	6.4	3102	2 T43291	laminin alpha chai
24	147.5	6.3	1801	1 MMRTS	laminin beta-2 cha
25	146.5	6.3	2531	2 T31070	notch homolog - se
26	146	6.3	277	2 A60771	B-cell activation
27	146	6.3	667	2 A48579	trophozoite surfac
28	145.5	6.3	416	1 JN0006	nerve growth facto
29	145	6.2	3635	2 T10053	laminin alpha 5 ch

30	144.5	6.2	326	1 GQVZML	T2 protein - myxom
31	144.5	6.2	1680	2 A43434	furin (EC 3.4.21.7
32	143.5	6.2	915	2 B48225	probable proptotei
33	143.5	6.2	4391	2 A38096	perlecan precursor
34	142	6.1	1557	2 T28811	hypothetical prote
35	141.5	6.1	686	2 JC7569	Delta-4 protein -
36	138.5	6.0	1299	2 T43251	furin (EC 3.4.21.7
37	138	5.9	271	2 S12783	OX40 antigen precu
38	138	5.9	305	2 A46476	B cell-associated
39	138	5.9	1607	1 MMMSB2	laminin gamma-1 ch
40	138	5.9	1609	1 MMHUB2	laminin gamma-1 ch
41	137.5	5.9	642	1 S52111	uromodulin precurs
42	137.5	5.9	1798	2 S53869	laminin beta-2 cha
43	136.5	5.9	260	1 A46517	CD27 antigen precu
44	136.5	5.9	2219	2 T27684	hypothetical prote
45	136.5	5.9	3712	2 S18253	laminin alpha-1 ch

ALIGNMENTS

RESULT 1

JC4302
tumor necrosis factor receptor p55 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C:Accession: JC4302; PC4093
R:Suter, B.; Pauli, U.
Gene 163, 263-266, 1995
A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
A:Reference number: JC4302; MUID:96011645; PMID:7590278
A:Accession: JC4302
A:Molecule type: mRNA
A:Residues: 1-461 <SUT>
A:Cross-references: UNIPROT:P50555; UNIPARC:UPI00001372A9; GB:U19994; NID:G1141752; PIDN
A:Accession: PC4093
A:Molecule type: protein
A:Residues: 1-7 <SU2>
A:Cross-references: UNIPARC:UPI0000176767
A:Experimental source: kidney cell line 15
C:Genetics:
A:Gene: tnfr
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homologs
C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-461/Product: tumor necrosis factor receptor p55 #status predicted <WAT>
F:44-194/Domain: extracellular cysteine rich #status predicted <EXT>
F:44-82/Domain: NGF receptor repeat homology <NGF>
F:84-126/Domain: NGF receptor repeat homology <NGF>
F:211-231/Domain: transmembrane #status predicted <TMW>
F:361-447/Domain: signal transduction #status predicted <SIT>
F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	17.9%	Score	415;	DB	2;	Length	461;
Best Local Similarity	30.5%	Pred.	No. 8.7e-21;				
Matches	140;	Conservative	44;	Mismatches	201;	Indels	74;
							Gaps 18;
QY	11	VAAALLVLLGARAQ	-----GTRSPR-----	CDACAGDFHKKIGLFCRCGCPAGHYLKAPCT	62		
DB	14	VLRALLVDVYPAGVHGLVLPDGRKRESLCPQGGKYSHPNRSICCTCKHGYLLNDCL	73				
QY	63	BPCGNSTCLVCPQDTFFLAWENHNHSEACQACDEQASVALENCSSAVADTRCGCKPGWF	122				
DB	74	GFGLDTRDCRENGIFTASEN-HLTQCLSCSKRSEMSQVEISPTVDRDTVCGCRKN--	130				
QY	123	VBCQSVQCVSSPFFCQPCDCLGALHRRHRLIC-SRRDTCGTCLPGFVEHGDGCVSCPT	181				
DB	131	---QVRKYWSETLFOCLNGLCP--NGTVQLPCLEKQDTIC-NCHSGFFLRKDEKVCVCVN	184				
QY	182	STLGSCPERCAVCGWRQMF-----WVQLLAGLVVPLLLGATLTVTYRHCWPH---	230				
DB	185	CKNADCKNLCPATSETRNDQDTGTTVLPVLVIFGLCLAFFLVGLACKYQKWKPKLYS	244				

QY 231 -----KPLVTADEAGMEALTPPPATHLSPLD--SAHTILLAPDSEKICTV 274
Db 245 IICGKSTPVKEGPEPLATAPSG-----PITTFSPISPSPTTTFSPVPSPISPP 297
QY 275 QLVGNSWT---PGVPETQALCQVWTSWDLPSRALGPAATLSP-----ESPAG 323
Db 298 TFTPQWSNIKVTSPPKEIAPPQAG-----PILPMPASTPTVPTPLPKWGGSAHSAHS 352
QY 324 SPAMQLQGP-QLYDVMDVAPARWKEFVFTLGLREAEIEAVEVEIGR-FRDOQYEMLKR 381
Db 353 AQAQLADADPATLYAVVDGVPPTKWEFVRLGLGHEIERLELQNGRCUREAQYSLAE 412
QY 382 WRQ---QQPAGLAVAAALERMGLDGCVEDLRSLRQGP 417
Db 413 WRRTSREATLELGSVLRMDMLGCLDIEAL-RGP 450
RESULT 2
QMSST1
tumor necrosis factor receptor 1 precursor - mouse
N;Alternate names: tumor necrosis factor receptor, 55K
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004
A;Accession: A38634; B40254; S16677; S19021; I54532; I57826
R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor
A;Reference number: A38634; MUID:91187885; PMID:1849278
A;Accession: A38634
A;Molecule type: mRNA
A;Residues: 1-454 <LEW>
A;Cross-references: UNIPROT:P25118; UNIPARC:UPI000002348D; GB:M60468; NID:g199825; PIDN:
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
A;Reference number: A40254; MUID:91246168; PMID:1645445
A;Accession: B40254
A;Molecule type: mRNA
A;Residues: 1-454 <GO2>
A;Cross-references: UNIPARC:UPI000002348D; GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:
R;Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissenberghis, A.M.; Gray, P.W.; Feildma
Eur. J. Immunol. 21, 1649-1656, 1991
A;Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis
A;Reference number: S16677; MUID:91285014; PMID:1647956
A;Accession: S16677
A;Molecule type: mRNA
A;Residues: 1-454 <BAR>
A;Cross-references: UNIPARC:UPI000002348D; EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:
R;Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
Immunogenetics 34, 338-340, 1991
A;Title: Molecular cloning and expression of the mouse Tnf receptor type b.
A;Reference number: S19021; MUID:92039815; PMID:1657766
A;Accession: S19021
A;Molecule type: mRNA
A;Residues: 1-454 <ROT>
A;Cross-references: UNIPARC:UPI000002348D; EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:
R;Babo, B.F.
Immunogenetics 39, 450-451, 1994
A;Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell
A;Reference number: I54532; MUID:94245292; PMID:8188324
A;Accession: I54532
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-454 <RES>
A;Cross-references: UNIPARC:UPI000002348D; GB:I26349; NID:g430732; PIDN:AAAS9361.1; PID:
R;Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
Mol. Immunol. 30, 165-176, 1993
A;Title: Genomic organization and promoter function of the murine tumor necrosis factor
A;Reference number: I57826; MUID:93156721; PMID:8381516
A;Accession: I57826
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-393,'G',395-454 <RE2>

A;Cross-references: UNIPARC:UPI0000161D7C; GB:M76656; NID:g202100; PIDN:AAA40465.1; PID:
C;Comment: This protein is one of two distantly related receptors for both TNF-alpha (cachectin) and
C;Gene: TNFR-2
A;Gene: TNFR-2
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C;Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F;30-212/Domain: extracellular #status predicted <EXT>
F;44-82/Domain: NGF receptor repeat homology <NG1>
F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-204/Domain: NGF receptor repeat homology <NG4>
F;213-235/Domain: transmembrane #status predicted <MEM>
F;236-454/Domain: intracellular #status predicted <INT>
F;54,151,202/Binding site: carbohydrate (Asn) #status predicted
Query Match 17.4%; Score 404.5; DB 1; Length 454;
Best Local Similarity 27.2%; Pred. No. 4.4e-20;
Matches 127; Conservative 56; Mismatches 191; Indels 93; Gaps 18;
QY 11 VAAALLLVILGARAQGGT-----RSPKDCAGDFHKIGLFCRCGCPAGHYLKA 59
Db 11 LSLVLLALLMGHPSGVGTGLVPSLGLDREKRDLSLCPQCKYVHSKNSICTCTCKHGTLYVS 70
QY 60 PCTPCGNSLTVCPQDTFLAVENHNSCARCQACQEQASQVALENCSAVADTRCGCKP 119
Db 71 DCPSGRDVTVCRCERKGTFTASQNYLR-QCLSKCTCKKMSQVEISPCQADKDTVCCK- 128
QY 120 GWFEVCQVQCVSSSPFYQCPCLDCCALHRTLLCSRRDTCGTCPLGYEHDGCVSC 179
Db 129 ----ENQFQRYLSETHFCQVDCSPC--FNGTVPICKETQNTVCNCHAGFLRESECVPC 182
QY 180 PYSLGLSCP--ERCAAVC-----GWRQMFVQVLLAGLVVPLLGLATLYTY 224
Db 183 ----SHCKKNECMKLCPLPPLAVNTVPQDSGTAVLLPLVLLGLCLLSFIFISLMCRY 237
QY 225 RHQWP-----HKPLVTADEAGMEALTPPPATHLSPLDSAHTLL-----APPSSEK 270
Db 238 PRWRPEVYIICNDPVPVKEKAGKELTAPSPAFSTSGFNTLGFSPGFSPPVSSSTP 297
QY 271 ICTVQLVGNWSW-----TPGY-PETQALC----PQVTSWDLPSRALGPAAP 314
Db 298 ISPI-FGPSNWHFMPVSEVVPVTOGADPLLYESLCSVPAPTSVQKWED----- 344
QY 315 TLPSPSPAGSPAMLOPQGLQDYMVAVPARWKEFVFTLGLREAEIEAVEVEIGR-FRD 373
Db 345 SAHPQRPDNLAL-----LYAVDGVPPARWKEFVFTLGLREAEIEAVEVEIGR-FRD 398
QY 374 QQYEMLKRVRQOQPA---GLGAVYAALERMGLDGCVEDLRSLRQGP 417
Db 399 AQYSMLAEAWRRTPRHEDTLEVVGLVLSKNLGLACLENLEAL-RNP 444
RESULT 3
QQRRT1
tumor necrosis factor receptor 1 precursor - rat
N;Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence revision 07-Oct-1994 #text change 09-Jul-2004
C;Accession: B36555
R;Himpler, A.; Maurer-Pogoy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;
DNA Cell Biol. 9, 705-715, 1990
A;Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor
A;Reference number: A36555; MUID:91090841; PMID:1702293
A;Accession: B36555
A;Molecule type: mRNA
A;Residues: 1-461 <HIM>
A;Cross-references: UNIPROT:P22934; UNIPARC:UPI00001372AA; GB:M63122; NID:g207361; PIDN:
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein

A;Molecule type: protein
A;Residues: 41-43,'X',45-53,'V',55-57,'XK',60 <OLS>
A;Cross-references: UNIPARC:UPI00001736E2
A;Experimental source: renal failure patient urine
R;Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
A;Reference number: A35010; MUID:90110215; PMID:2153136
A;Accession: A35010
A;Molecule type: protein
A;Residues: 41-45 <ENG>
A;Cross-references: UNIPARC:UPI00001736E3
A;Experimental source: normal urine
R;Kajihara, J.; Asada, A.; Kiriha, S.; Kato, K.
Biochim. Biotechnol. Biochem. 59, 2266-2268, 1994
A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified from human urine.
A;Reference number: JC2404; MUID:95128033; PMID:7765720
A;Accession: JC2404
A;Molecule type: protein
A;Residues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>
A;Cross-references: UNIPARC:UPI00001736E4
A;Experimental source: urine
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
C;Genetics:
A;Gene: GDB:TNFR1
A;Cross-references: GDB:125913; OMIM:191190
A;Map position: 12p13.2-12p13.2
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homologous
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-45/Domain: tumor necrosis factor receptor 1 #status predicted <MAT>
F;30-211/Domain: extracellular #status predicted <EXI>
F;41-201/Domain: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status predicted <INT>
F;44-82/Domain: NGF receptor repeat homolog <NG1>
F;84-126/Domain: NGF receptor repeat homolog <NG2>
F;127-167/Domain: NGF receptor repeat homolog <NG3>
F;168-196/Domain: NGF receptor repeat homolog <NG4>
F;212-234/Domain: transmembrane #status predicted <MEM>
F;235-455/Domain: intracellular #status predicted <INT>
F;54,145,151/Binding site: carbohydrate (Asn) #status predicted

Query Match 16.1%; Score 374; DB 1; Length 455;
Best Local Similarity 28.3%; Pred. No. 5e-18;
Matches 131; Conservative 49; Mismatches 183; Indels 100; Gaps 22;

QY 15 LLLVLLGARAQG-----GTRSPR---CDCAGDFHKIIGLPCRCGCPAGHYLKAPCTE 63
DB 15 LLELLVGIYPSGVIGLVPHLGDREKRDVCPQGYIHPQNNISCTCKCHKGTLYLNDGPG 74
QY 64 PCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASOVALENCASAVADTRCCKPGWFV 123
DB 75 PQQDTDCRECSGFTASENHLR-HCLSCSKCKEMGQVEISCTVDRTVCCGRKNQYR 133
QY 124 EC---QVSQCVSSPPFCQPCDGLGALHRRHTRLLCSRRDTCGTLPGFVEHGDGCVSCP 180
DB 134 HYSENILFQC-----FNCISCLIN-GTVH-----LSCQEKQNTVCTCHAGFLRENEVCSC- 192
QY 181 TSTLGSCEP---RCAAVC-----GWRQMFVQVLLAGLVPLLLGATLTYTRH 226
DB 183 ----SNCKKSLETKLCLPQIENVKGTEDSGTTVLLPLVIFGLCLLSLLFGLMYRYQR 238
QY 227 CWPHK-----PLVTADEAGMEALTPPPATHLSPLDS-----AHTLLAPDSSEKIC 272
DB 239 -WKSCLYSIVCGKSTPEKELEGSTTKP---LAPNPSFPTGFTPTLGFSPVPSSTFT 294
QY 273 TVQLVGNSTWTPGYPETQALCPQVTSWDLPSRALGSP-----AAAPTLS- 318
DB 295 S-----SSTYTPGD-----CPNFA-----APREVAAPPQGDPPILATLASDPPNPL 338
QY 319 ---ESPAGSPAMMLQPGP-QLYDMDAVPARRWKEFVTRTGLREARIEAVEVEIGR-FRD 373
DB 339 QKWEDSAHKPQSLDTPDDPATLYAVENVPLRWKEFVRRGLGLSDHEIDRLQNGRCLE 398

QY 374 QQYEMLKRWROQOP-----AGLGAVYAALERMGLDGCVEDLRSRL 413
DB 399 AQYSMLATWRRTPRREATLELLGRVLRDMDLGLCLEDIEEAL 441

RESULT 5
A40036
apoptosis-mediating surface antigen Fas precursor - human
N;Alternate names: surface antigen APO-1
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1992 #sequence revision 17-Jan-1992 #text_change 09-Jul-2004
C;Accession: A40036; S24543; A38142
R;Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; Hase, Cell 66, 233-243, 1991
A;Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can mediate apoptosis.
A;Reference number: A40036; MUID:91309137; PMID:1713127
A;Accession: A40036
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-335 <ITO>
A;Cross-references: UNIPROT:P25445; UNIPARC:UPI000003060C; GB:M67454; NID:g182409; PIDN:R;Krammer, P.H.
submitted to the EMBL Data Library, February 1992
A;Reference number: S24543
A;Accession: S24543
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-335 <KRA>
A;Cross-references: UNIPARC:UPI000003060C; EMBL:X63717; NID:g28741; PID:g28742
R;Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; Richter, J. Biol. Chem. 267, 10709-10715, 1992
A;Title: Purification and molecular cloning of the APO-1 cell surface antigen, a member of the TNF family.
A;Reference number: A38142; MUID:92268122; PMID:1375228
A;Accession: A38142
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-134,'Q',136-335 <OEH>
A;Cross-references: UNIPARC:UPI000014E7A3
A;Experimental source: SKW6.4 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:103810)
A;Note: in NCBI backbone the source is designated as mouse
C;Genetics:
A;Gene: GDB:APT1
A;Cross-references: GDB:132671; OMIM:134637
A;Map position: 10q24.1-10q24.1
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homologous
C;Keywords: apoptosis; surface antigen; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;85-128/Domain: NGF receptor repeat homolog <NG4>
F;174-190/Domain: transmembrane #status predicted <TMM>

Query Match 8.6%; Score 199.5; DB 2; Length 335;
Best Local Similarity 21.4%; Pred. No. 2.2e-06;
Matches 74; Conservative 43; Mismatches 106; Indels 123; Gaps 12;

QY 44 GLPCCGCGPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASOVA 103
DB 56 GQCHPCPCGGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFSKCRRCCLDCEGHGLEV 115
QY 104 LENCASAVADTRCCKPGWFVEQCVQSVSSPPFCQPCDGLGALHRRHTRLLCSRRDTCG 163
DB 116 EINCTRTQNTCKCKNFP-----CNSTVCEHCDPCTKC----- 149
QY 164 TCLPGFYEHGDGCVSCPTSTLGSCEPCARCAAVCGWR-OMFWVQVLLAGLVPLLLGATLTY 222
DB 150 -----EHGI-IKECTLTSTNTCKEE-----GSRNLGWLCLLL--LPILIVWVRKE 194
QY 223 TYRHCHWPHKPLVTADEAGMEALTPPPATHLSPLDSAHTL---LAPDSSEKICTVQLVGN 279
DB 195 VQKTCRKH-----KENQG-----SHESPTLNPTETVAINLSDVLSKYITTI----- 236
QY 280 SWTPGYPETQALCPQVTSWDLPSRALGSPAAAPTLSPESPAGSPAMMLQPGPOLYDVM 339

```

Biochem. Biophys. Res. Commun. 198, 666-674, 1994
A;Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat liver
A;Reference number: JC2395; MUID:94128114; PMID:7507668
A;Accession: JC2395
A;Molecule type: mRNA
A;Residues: 1-324 <KIM>
A;Cross-references: UNIPROT:Q63199; UNIPARC:UPI00001370ED; DBJ:D26112; NID:9468486; PID:
A;Experimental source: thymus
A;Accession: PC2246
A;Molecule type: mRNA
A;Residues: 1-62, 'RFT', <K12>
A;Cross-references: UNIPARC:UPI000011F885; DBJ:D26113; NID:9468488; PIDN:BAA05109.1; PII
A;Experimental source: liver
C;Genetics:
A;Introns: 62/1
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C;Keywords: transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-324/Product: Fas antigen #status predicted <NAT>
F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NG4>
F;171-188/Domain: transmembrane #status predicted <TM>

Query Match 7.5%; Score 175; DB 2; Length 324;
Best Local Similarity 28.5%; Pred. No. 9.6e-05;
Matches 43; Conservative 17; Mismatches 67; Indels 24; Gaps 5;

QY 11 VAAALLVLG-----ARAQG-----GTRSPRCDCAGDFHKKIGLFCRCGCPAG 54
DB 4 IMAVLPLVLGAPLNVRMGTDSIFGLKLRVRETNNCSGLY-QVGFPCQCPQG 62
QY 55 HYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDQASQVALENSAVADTR 114
DB 63 ERVKDCTTSGGAPTCPTCEGEEYTDKXYSKRCARCAFCDSGHGLEVEITCTRTQNTK 122
QY 115 CGCKPWFVEQVSCVSSPPYQPCLDG 145
DB 123 CRCKENFY--CNASLC-----DHCYHCTSCG 146

RESULT 8
I37383
FAS soluble protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I37383
R;Cascino, I.; Fiacuci, G.; Papoff, G.; Ruberti, G.
J. Immunol. 154, 2706-2713, 1995
A;Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule are
A;Reference number: I37383; MUID:95181785; PMID:7533181
A;Accession: I37383
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-314 <RES>
A;Cross-references: UNIPROT:P25445; UNIPARC:UPI000002B592; EMBL:Z47993; NID:9728578; PID
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog

Query Match 7.2%; Score 168; DB 2; Length 314;
Best Local Similarity 19.1%; Pred. No. 0.00028;
Matches 66; Conservative 37; Mismatches 100; Indels 142; Gaps 10;

QY 44 GLFCCRCGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDQASQVA 103
DB 56 GQFCHKPCPPGERKARDCTVNGDEPCVQCEGKEYTDKRAHFSKCRCLCDGEGHGLEV 115
QY 104 LENCASAVADTRCGCKPWFVEQVSCVSSPPYQPCLDGALHRRHRLLCRRRDTDCG 163
DB 116 EINCTRTQNTKCRCKDNFF-----CNSTVCSHCDPCTKC----- 149
QY 164 TCLPGFYHGDGCVSCPTSTLGSCTPCRCACVCCWRQFWQVLLAGLVLPVLLGATLTYT 223
DB 150 -----EHGI-IKECTLTSTNCKSE-----VKKEV 174

apoptosis-mediating membrane-associated polypeptide Fas - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46484; A47254
R;Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenkins,
J. Immunol. 148, 1274-1279, 1992
A;Title: The cDNA structure, expression, and chromosomal assignment of the mouse Fas ant
A;Reference number: A46484; MUID:92148151; PMID:1371136
A;Accession: A46484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-327 <NAT>
A;Cross-references: UNIPROT:P25446; UNIPARC:UPI0000027457; GB:M83649; NID:91932225; PIDN:
A;Experimental source: BAW3 macrophage cell line
A;Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBIIP:81545)
R;Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993
A;Title: Aberrant transcription caused by the insertion of an early transposable element
A;Reference number: A47254; MUID:93189556; PMID:7680478
A;Accession: A47254
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-96 <ADA>
A;Cross-references: UNIPARC:UPI0000170C50; GB:S56490; NID:9298505; PIDN:AAB25700.1; PID:
A;Experimental source: MRL lpr/lpr
A;Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:126863,
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C;Keywords: transmembrane protein
F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NG4>

Query Match 8.4%; Score 196; DB 2; Length 327;
Best Local Similarity 23.8%; Pred. No. 3.7e-06;
Matches 62; Conservative 25; Mismatches 109; Indels 64; Gaps 8;

QY 13 AALLVLGARAQGTSPRC-----DCAGDFHKKIGLFCRCGCPAGHY 56
DB 6 AVLPLVLGASQLRVHTQGTNSISESLKLRVRVHETDKNCSEGLYQG-GPCCQCPQPKK 64
QY 57 LKAPCTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDQASQVALENSAVADTRCG 116
DB 65 KVEDCKWNGTPTCAPCTEKEKYMDKHYADKRCRCLCDEHGLEVEITCTLTQNTCK 124
QY 117 CKPWFVEQVSCVSSPPYQPCLDGALHRRHRLLCRRRDTDCGTCPLPGFYHGDGC 176
DB 125 CKP-----DFYCDSE-----PG-CEHCVRG 142
QY 177 VSCPTSTLGSCTPCRCACV---GWRQFWQVLLAGLVLPVLLGATLTYTYRHCWPKPL 233
DB 143 ASCEHGTLEPTATSTNCRKQSPNRLWLLTLV-LLIPLVP-IVRYKRRKRCWRQD 200
QY 234 VTADAGMEALTPPPATHLS 253
DB 201 DPESRTSSRETIPWNASNLS 220

RESULT 7
JC2395
Fas antigen precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: JC2395; PC2246
R;Kimura, K.; Wakatsuki, T.; Yamamoto, M.
```


MEGF6 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13954
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 54, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: Z14126; MUID:98360089; PMID:9693030
A;Accession: T13954
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1574 <NAK>
A;Cross-references: UNIPROT:O88281; UNIPARC:UPI0000043BEE; EMBL:AB011532; NID:g3449293;
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Gene: MEGF6

Query Match 6.8%; Score 158; DB 2; Length 1574;
Best Local Similarity 24.5%; Pred. No. 0.0061;
Matches 90; Conservative 16; Mismatches 120; Indels 142; Gaps 23;

QY 30 SPRDCAGDHHKIGLFCRCGPAGHY-----LKAPCTEPCGNSTCLV----- 72
Db 933 SGACTCPAGWR---GSFCEHACAGFGLDCLDSACNSGAPCDVATGSCICPAGRWGPR 989

QY 73 ----CPQDTFLAWENHNHNSCARCOACDEQASOALENCNSAVADTRCGCKPGWF----- 122
Db 990 CAQSCPLTF-----GLNCSQICTCFNGAS-----CDSVTG-QCHCAPGWMGPTCLQ 1035

QY 123 -----VSCQVSSQVSSPFFCQCL-DCGALHRRLLCSRRDPTDCTCLPGFVE-- 171
Db 1036 ACPPGLYKNCQHS-CLCRNGRGCDPTLGQCTCEGWTGLACENE-----CLPGHYAAG 1088

QY 172 -----HGDGC-----VSCPTSLG-SCPERCA-----AVC----- 195
Db 1089 COLNCSCLHGGICDRLTGHCLCPAGWTGDKQSCSCVSGTFGVHCEHCACRKGASCHVT 1148

QY 196 -----GWRQMFVQVLLAGLVVLLLGATLTVTYRHCPHPLVTVADAGMEALTPPP 248
Db 1149 GACFCPPGWRGPHCEQACPRGWEACACRCLCPFNASC--HH--VTG-----ECRCPPG 1199

QY 249 ATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTWPG-YPETQAL--CPQVTVSWDQLPS 305
Db 1200 FTGL-----SCEQAC-----QPGTFGKDCHELCQCPGETWACD--PA 1234

QY 306 RALGPAA 313
Db 1235 SGVCTCAA 1242

RESULT 15
QHUN
nerve growth factor receptor precursor, low affinity [validated] - human
N;Alternate names: NGF receptor
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: A25218; A60204; S21689; I57638
R;Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.
Cell 47, 545-554, 1986
A;Title: Expression and structure of the human NGF receptor.
A;Reference number: A25218; MUID:87051725; PMID:3022937
A;Accession: A25218
A;Molecule type: mRNA
A;Residues: 1-427 <JOH>
A;Cross-references: UNIPROT:P08138; UNIPARC:UPI0000049854; GB:M14764; NID:g189204; PIDN:
R;Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schattelman, G.; Thompson, S.; Grob, P.;
J. Neurochem. 48, 225-232, 1987
A;Title: Purification and amino terminal sequencing of human melanoma nerve growth factor
A;Reference number: A60204; MUID:87085574; PMID:3025363
A;Accession: A60204
A;Molecule type: protein
A;Residues: 29-31, 'T', 33-42, 'TT', 45-46, 'TK', 50-51, 'XX', 54-56 <MAR>
A;Cross-references: UNIPARC:UPI00001736DA

A;Experimental source: melanoma cell line A875
A;Note: this sequence has been corrected by a note added in proof to follow the nucleotide
R;Visnavajjhala, P.; Lezyk, J.D.; Lin-Goerke, J.; Ross, A.H.
Arch. Biochem. Biophys. 294, 244-252, 1992
A;Title: Structural domains of the extracellular domain of human nerve growth factor rec
A;Reference number: S21689; MUID:92198017; PMID:1372492
A;Accession: S21689
A;Status: preliminary
A;Molecule type: protein
A;Residues: 183-208 <VIS>
A;Cross-references: UNIPARC:UPI00001736DB
R;Sehgal, A.; Patil, N.; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
A;Title: A constitutive promoter directs expression of the nerve growth factor receptor
A;Reference number: I57638; MUID:89096903; PMID:2850481
A;Accession: I57638
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-22 <RES>
A;Cross-references: UNIPARC:UPI000016ADDE; GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma ce
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of t
C;Comment: This protein is thought to form a high-affinity receptor when it associates w
C;Comment: This receptor undergoes both N- and O-linked glycosylation.
C;Genetics:
A;Gene: GDNF/NGFR
A;Cross-references: GDB:120234; OMIM:162010
A;Map position: 17q21-17q22
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-427/Product: nerve growth factor receptor #status experimental <NAT>
F;29-250/Domain: extracellular #status predicted <EXT>
F;32-65/Domain: NGF receptor repeat homology <NG1>
F;67-108/Domain: NGF receptor repeat homology <NG2>
F;109-147/Domain: NGF receptor repeat homology <NG3>
F;149-189/Domain: NGF receptor repeat homology <NG4>
F;197-248/Region: serine/threonine-rich
F;251-272/Domain: transmembrane #status predicted <TRM>
F;273-427/Domain: intracellular #status predicted <INT>
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.7%; Score 155.5; DB 1; Length 427;
Best Local Similarity 22.1%; Pred. No. 0.0026;
Matches 104; Conservative 36; Mismatches 191; Indels 139; Gaps 21;

QY 15 LLLVLGARAQGGTRSPRCDAGDFHKKTGLFCRCGPAGHYLKAPC-----TEPCGNS 68
Db 16 LLLLLLGV-SLGGAKEA---CPTGLYTHSG-ECCACNLGEGVAQPCGANQTVCEPCLDS 70

QY 69 TCLVCPQDTFLAWENHNHNSCARCOACDEQASOALENCSA-----VADTRCGCKPGWFE 124
Db 71 ----VTFSDVVVSAT-----PKPCTEC-----VGLQSMSPAPCVCEADDAVCRCAVGYQD 116

QY 125 -----CQVSCQVSSPFFCQCLDCGALHRRLLCSRRDPTDCTCLPGFY-----EH 172
Db 117 ETTGRCEACRCVCEAGSLGVFSQ-----DKQNTVCECPDGTYSDEANH 160

QY 173 GDGCVSCPT-----STLGSQPCERCAVCGWRQMFVQVLLAGLVVLLLGATLTYYTRHC 227
Db 161 VDFCLPCTVCEDTERTQRECTRWADAECEIPIGRWIT----- 197

QY 228 WPHKPLVTADAGMEALTP--PPATHLSPLDSAHLLAPPDSSEKICTVOLVGNSTWPGY 285
Db 198 -RSTPEGSDSTAPSTQEPPEAPPEQDLIASTVAGVTVTWGSSQPVVTRGTTN-LIPVY 255

QY 286 PETQEAL-----CPQVTVSWDQLPSRALGFPAAAPTLSPESPAGSPAMML- 329
Db 256 CSLAAVVVLGVAYIAFKRWNSCKQKQGANSEFVNPQTPPEGEKLSHDSGISVDSQSLH 315

QY 330 --QPGQ-----LYVMDAVPARR-----WKFFVTLGLREAEI 361
Db 316 DQOPHTQTASGQALKGDGGLYSSLP--PAKREVEVKLLNGSAGDTWRHLAAGELGYOPEHI 373

QY 362 EAVEVEIGRPRDQOYEMLKWRQOPAGLCAVYAALERMGLDGCVEDLRS 411
Db 374 DSFTHEACPVR-----ALLASNATQDSATLDALLAALRRRIQORADLIVESLCS 419

Search completed: March 20, 2006, 08:00:01
Job time : 29 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 07:59:11 ; Search time 110 Seconds
(without alignments)
2674.594 Million cell updates/sec

Title: US-10-081-280-6

Perfect score: 2323

Sequence: 1 MEQPRGCAVAAALLVLL.....ERMGLDGCVEDLSRLQGRP 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2323	100.0	417	1	TNR25 HUMAN
2	2323	100.0	417	2	Q5T8X6 homo sapien
3	2312.5	99.5	418	2	Q5T8X7 homo sapien
4	2196.5	94.6	426	2	Q5T8X5 homo sapien
5	1397	60.1	413	2	Q99MM1 mus musculus
6	1255	54.0	387	2	Q8VD70 mus musculus
7	1164	50.1	253	2	Q5T8X3 HUMAN
8	1066.5	45.9	215	2	Q5T8X4 homo sapien
9	1054	45.4	277	2	Q5T8X8 HUMAN
10	1036	44.6	178	2	Q5T8X2 HUMAN
11	415	17.9	461	1	TNR1A_PIG
12	406.5	17.5	440	2	Q6QHFO MOUSE
13	405.5	17.5	440	2	Q6QH2 MUSSP
14	404.5	17.4	440	2	Q6QH1 MOUSE
15	404.5	17.4	454	1	TNR1A MOUSE
16	403.5	17.4	461	2	Q5UIX6 RAT
17	394.5	17.0	461	1	TNR1A RAT
18	387.5	16.7	471	1	TNR1A BOVIN
19	374	16.1	455	1	TNR1A HUMAN
20	365	15.7	446	2	Q95ND3 FELCA
21	323.5	13.9	427	2	Q5ZJG1_CHICK
22	293.5	12.6	386	2	Q4SND9_TETNG
23	247.5	10.7	332	1	TNR6_PIG
24	241.5	10.4	302	2	Q4SNE8_TETNG
25	226	9.7	319	2	Q4TV79_RABIT
26	224.5	9.7	313	2	Q4G265 HORSE
27	223.5	9.6	389	2	Q6NUU6_BRARE
28	221	9.5	314	2	Q861W6 FELCA
29	217.5	9.4	320	2	Q9XS29_RABIT
30	214.5	9.2	328	2	Q76B99_XENLA
31	211.5	9.1	328	2	Q6GL24_XENLA

RESULT 1

ID	TNR25 HUMAN	STANDARD	PRT:	417 AA.
AC	Q93038	Q00275; Q00277; Q00278; Q00279; Q00280; Q14865;		
AC	Q14866	P78507; P78515; Q92983; Q93036; Q93037; Q99722; Q99830;		
AC	Q99831	Q9BY86; Q9UM80; Q9UME1; Q9UME5;		
DT	01-NOV-1997	(Rel. 35, Created)		
DT	13-SEP-2005	(Rel. 48, Last sequence update)		
DE	Tumor necrosis factor receptor superfamily member 25 precursor (WSL-1 protein) (Apoptosis-mediating receptor DR3) (Apoptosis-mediating receptor TRAMP) (Death domain receptor 3) (WSL protein) (Apoptosis inducing receptor AIR) (Apo-3) (lymphocyte associated receptor of death) (LARD)			
GN	Name=TNFRSF25; Synonyms=APO3, DDR3, DR3, TNFRSF12, WSL, WSL1;			
GN	ORFNames=UNQ455(Pro779;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE (ISOFORMS 1; 3 AND 4), AND MUTAGENESIS.			
RC	TISSUE=Lymphoid;			
RX	MEDLINE=97088617; PubMed=8934525; DOI=10.1038/384372a0;			
RA	Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T., Grinham C.J., Brown R., Farrow S.N.;			
RT	"A death-domain-containing receptor that mediates apoptosis.";			
RL	Nature 384:372-375 (1996).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE (ISOFORM 1).			
RC	TISSUE=Umbilical vein endothelial cell;			
RX	MEDLINE=97081063; PubMed=8875942; DOI=10.1126/science.274.5289.990;			
RA	Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M., Duan D.R., King L., Gentz R., Ni J., Dixit V.M.;			
RT	"Signal transduction by DR3, a death domain-containing receptor related to TNFR-1 and CD95.";			
RL	Science 274:990-992 (1996).			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;			
RL	Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RC	TISSUE=Heart;			
RX	MEDLINE=97148200; PubMed=8994832; DOI=10.1016/S0960-9822(02)70791-4;			
RA	Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L., Goddard A.D., Bauer K.D., Ashkenazi A.;			
RT	"Apo-3, a new member of the tumor necrosis factor receptor family, contains a death domain and activates apoptosis and NF-kappa-B.";			
RL	Curr. Biol. 6:1669-1676 (1996).			
RN	[5]			
RP	NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9 AND 10).			
RX	MEDLINE=97272273; PubMed=9114039; DOI=10.1073/pnas.94.9.4615;			

ALIGNMENTS

Q92956 homo sapien
Q61B95 homo sapien
Q9dfv0 brachydanio
O57408 melesgrie g
O14763 homo sapien
Q6fh58 homo sapien
Q9xs28 cercopithec
Q9qz24 mus musculu
P25445 homo sapien
Q6ict6 homo sapien
Q5t9p1 homo sapien
Q5t9f8 homo sapien
Q9iar7 gallus gall
Q95185 felis alive

TNR14_HUMAN
Q61B95_HUMAN
Q9DFV0_BRARE
O57408_MELGA
TR10B_HUMAN
Q6FH58_HUMAN
Q9XS28_CERAE
TR10B_MOUSE
TNR6_HUMAN
Q6ICT6_HUMAN
Q5T9P1_HUMAN
Q5T9F8_HUMAN
Q9IAR7_CHICK
Q95185_FELCA

283
283
438
368
440
440
283
381
335
335
335
362
368
189

8.9
8.9
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8.6
8.5

206.5
206.5
205
203.5
203.5
203.5
200.5
200
199.5
199.5
199.5
199.5
199.5
198

RA Screenshot G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,
RA McMichael A.J., Bell J.I.;
RT "LARD: a new lymphoid-specific death domain containing receptor
RT regulated by alternative pre-mRNA splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
RN [6]
RP NUCLEOTIDE SEQUENCE (ISOFORMS 11 AND 12).
RX MEDLINE=98113360; PubMed=9446802; DOI=10.1006/bbrc.1997.7948;
RA Warzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B.,
RA Salles G.;
RT "A new death receptor 3 isoform: expression in human lymphoid cell
RT lines and non-Hodgkin's lymphomas.";
RL Biochem. Biophys. Res. Commun. 242:376-379(1998).
RN [7]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1), AND VARIANT GLY-159.
RA Shiozawa S., Konishi Y., Murayama K., Mukae N., Yamamoto E.,
RA Hayashi S., Sato M., Shiozawa K., Tsukamoto Y.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [8]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hase P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seahagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wicand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.M.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [9]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS GLN-23; GLY-159 AND
RP ARG-254.
RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witak L.A., Nickerson D.A.;
RT "NIH-SNPs, environmental genome project, NIHES ES15478, Department
RT of Genome Sciences, Seattle, WA [URL: <http://egp.gs.washington.edu>].";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [10]
RP NUCLEOTIDE SEQUENCE OF 4-417.
RC TISSUE=Brain, and Fetal lung;
RX MEDLINE=97205335; PubMed=9052839;
RA Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
RA Thome M., Bornand T., Hahne M., Schroeter M., Wilson A., French L.E.,
RA Browning J.L., Macdonald H.R., Tschopp J.;
RT "TRAMP, a novel apoptosis-mediating receptor with sequence homology to
RT tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";
RL Immunity 6:79-88(1997).
RN [11]
RP NUCLEOTIDE SEQUENCE OF 7-417.
RC TISSUE=Brain;
RA Chaudhary P.M., Hood L.E.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [12]
RP INTERACTION WITH BAG4.
RX MEDLINE=99115917; PubMed=9915703; DOI=10.1126/science.283.5401.543;
RA Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;
RT "Prevention of constitutive TNF receptor 1 signaling by silencer of
RT death domains.";
RL Science 283:543-546(1999).
RN [13]
RP SPLICING ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA Hillman R.T., Green R.E., Brenner S.E.;
RT "An unappreciated role for RNA surveillance.";
RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
CC -1- FUNCTION: Receptor for TNFSF12/APO3L/TWEAK. Interacts directly
CC with the adapter TRADD. Mediates activation of NF-kappa-B and

induces apoptosis. May play a role in regulating lymphocyte
homeostasis.
-1- SUBUNIT: Homodimer. Interacts strongly via the death domains with
TNFRSF1 and TRADD to activate at least two distinct signaling
cascades, apoptosis and NF-kappa-B signaling. Interacts with BAG4.
-1- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 2, 9
and 11); Secreted (isoforms 3, 4, 5, 6, 7, 8, 10 and 12)
(Potential).
-1- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=12;
Name=1; Synonyms=WSL-1, LARD-1A;
IsoId=Q93038-1; Sequence=Displayed;
Name=2; Synonyms=LARD-1B;
IsoId=Q93038-2; Sequence=VSP_006504;
Name=3; Synonyms=WSL-S1, LARD-3;
IsoId=Q93038-3; Sequence=VSP_006497, VSP_006498;
Note=May be produced at very low levels due to a premature stop
codon in the mRNA, leading to nonsense-mediated mRNA decay;
Name=4; Synonyms=WSL-S2, LARD-2;
IsoId=Q93038-4; Sequence=VSP_006501, VSP_006502;
Note=May be produced at very low levels due to a premature stop
codon in the mRNA, leading to nonsense-mediated mRNA decay;
Name=5; Synonyms=LARD-4, LARD-11;
IsoId=Q93038-5; Sequence=VSP_006495;
Note=May be produced at very low levels due to a premature stop
codon in the mRNA, leading to nonsense-mediated mRNA decay;
Name=6; Synonyms=LARD-5;
IsoId=Q93038-6; Sequence=VSP_006491, VSP_006495;
Note=May be produced at very low levels due to a premature stop
codon in the mRNA, leading to nonsense-mediated mRNA decay;
Name=7; Synonyms=LARD-6;
IsoId=Q93038-7; Sequence=VSP_006491, VSP_006493, VSP_006494;
Note=May be produced at very low levels due to a premature stop
codon in the mRNA, leading to nonsense-mediated mRNA decay;
Name=8; Synonyms=LARD-7;
IsoId=Q93038-8; Sequence=VSP_006492;
Name=9; Synonyms=LARD-8;
IsoId=Q93038-9; Sequence=VSP_006491;
Name=10; Synonyms=LARD-9;
IsoId=Q93038-10; Sequence=VSP_006503;
Name=11; Synonyms=Beta;
IsoId=Q93038-11; Sequence=VSP_006496;
Name=12; Synonyms=Beta soluble;
IsoId=Q93038-12; Sequence=VSP_006499, VSP_006500;
Note=May be produced at very low levels due to a premature stop
codon in the mRNA, leading to nonsense-mediated mRNA decay;
-1- TISSUE SPECIFICITY: Abundantly expressed in thymocytes and
lymphocytes. Detected in lymphocyte-rich tissues such as thymus,
colon, intestine, and spleen. Also found in the prostate.
-1- PTM: Glycosylated (Probable).
-1- SIMILARITY: Contains 1 death domain.
-1- SIMILARITY: Contains 4 TNFR-Cys repeats.
-1- CAUTION: Ref.5 reports for isoform 4 at position 208 a serine
residue instead of arginine.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

EMBL; Y09392; CAA70561.1; -; mRNA.
EMBL; Y09392; CAA70559.1; -; mRNA.
EMBL; Y09392; CAA70560.1; -; mRNA.
EMBL; U72763; AAC50819.1; -; mRNA.
EMBL; U83599; AAB41434.1; -; Genomic DNA.
EMBL; U83600; AAB41435.1; -; Genomic RNA.
EMBL; U78029; AAB40918.1; -; mRNA.
EMBL; U74611; AAB39714.1; -; mRNA.
EMBL; U94501; AAC51306.1; -; mRNA.
EMBL; U94504; AAC51309.1; -; mRNA.
EMBL; U94502; AAC51307.1; -; mRNA.
EMBL; U94503; AAC51308.1; -; mRNA.

121	QY	WFVEQVSCQVSSPPYQPCDCLDGGALHRRHRLTLLCSRDDTCGTCLPGFVEHGGCVSCP	180
121	Db	WFVEQVSCQVSSPPYQPCDCLDGGALHRRHRLTLLCSRDDTCGTCLPGFVEHGGCVSCP	180
181	QY	TSTLGSCEPCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCMWPKHPLVTADEAG	240
181	Db	TSTLGSCEPCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTYRHCMWPKHPLVTADEAG	240
241	QY	MEALTTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNWNTPGYPETOEALCPQVTTWSW	300
241	Db	MEALTTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNWNTPGYPETOEALCPQVTTWSW	300
301	QY	DQLPSALGPAAAPTLLSPSPAGSPAMWLQPGPOLYDVMDAVPARRWKEFVRTILGLREAE	360
301	Db	DQLPSALGPAAAPTLLSPSPAGSPAMWLQPGPOLYDVMDAVPARRWKEFVRTILGLREAE	360
361	QY	IEAVEVEIGFRDQOQYEMLKWRRQOQAPAGLGVAAALERMGLDGCVDLRSRLQGP	417
361	Db	IEAVEVEIGFRDQOQYEMLKWRRQOQAPAGLGVAAALERMGLDGCVDLRSRLQGP	417

RESULT 3

Q5T8X7	HUMAN	
ID	Q5T8X7	HUMAN PRELIMINARY; PRT; 418 AA.
AC	Q5T8X7;	
DT	01-FEB-2005	(TEMBLrel. 29, Created)
DT	01-FEB-2005	(TEMBLrel. 29, Last sequence update)
DT	01-FEB-2005	(TEMBLrel. 29, Last annotation update)
DE	Tumor necrosis factor receptor superfamily, member 25 (Fragment).	
DE	GN=TNFRSP25; ORFNames=RP4-650H14.2-005;	
GN	Homo sapiens (Human).	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;	
OC	Homo.	

[illegible]

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Db 301 WDQLPSRALGPAAAPTLLSPSPAGSPAMMLQPGQLYDVMADVARRKWEFVRTIGLREA 360
Qy 360 EIEAVEVEIGRFRDQOQYEMLKRWRQOQAGLGAIVAAALERMGLDGCVEDLRSR 417
Db 361 EIEAVEVEIGRFRDQOQYEMLKRWRQOQAGLGAIVAAALERMGLDGCVEDLRSR 418

RESULT 4
Q5T8X5_HUMAN
ID Q5T8X5_HUMAN PRELIMINARY; PRT; 426 AA.
AC Q5T8X5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 25.
GN Name=TNFRSF25; ORFNames=RP4-650H14.2-004;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Glithero R.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL158217; CA122155.1; -; Genomic DNA.
DR GO: GO:0005515; F:protein binding; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR000488; Death.
DR InterPro: IPR006209; EGF like.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; Death; 1.
DR Pfam: PF00020; TNFR_c6; 1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS0017; DEATH DOMAIN; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00050; TNFR_NGFR_2; 1.
DR KJ Receptor.
SQ SEQUENCE 426 AA; 45927 MW; 292A9B2899F3AE1F CRC64;

Query Match 94.68; Score 2196.5; DB 2; Length 426;
Best Local Similarity 94.68; Pred. No. 4.5e-144;
Matches 403; Conservative 3; Mismatches 11; Indels 9; Gaps 3;

Qy 1 MEQRPRCAAVAAALLVLLGARAQGGTRSPRCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQRPRCAAVAAALLVLLGARAQGGTRSPRCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTBPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCASVADTRCGCKPG 120
Db 61 CTBPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCASVADTRCGCKPG 120

Qy 121 WFVECVQSVSSPFYQCPCLDCGALHRTLLCSRRDTCGTCLPFGFHEHGDGVCSP 180
Db 121 WFVECVQSVSSPFYQCPCLDCGALHRTLLCSRRDTCGTCLPFGFHEHGDGVCSP 180

Qy 181 T--STLGSCEPERCA-----AVCCWR--QMFVQVQLLAGLVVPLLAGLTYTYRHCHWPHK 231
Db 181 TPPSLAGAPGAVQSAVPLSVAGRGVGVFVQVQLLAGLVVPLLAGLTYTYRHCHWPHK 240

Qy 232 PLVTADAGMEALTPPPATHLSPLDSAHLLAPPDSSEKI CTVOLVNSWTPGYPETQEA 291
Db 241 PLVTADAGMEALTPPPATHLSPLDSAHLLAPPDSSEKI CTVOLVNSWTPGYPETQEA 300

Qy 292 LCPQVTSWQDLSRALGPAAAPTLLSPSPAGSPAMMLQPGQLYDVMADVARRKWEFV 351
Db 301 LCPQVTSWQDLSRALGPAAAPTLLSPSPAGSPAMMLQPGQLYDVMADVARRKWEFV 360

Qy 352 RTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWRQOQAGLGAIVAAALERMGLDGCVEDLRS 411
Db 361 RTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWRQOQAGLGAIVAAALERMGLDGCVEDLRS 420

RESULT 5
Q99MM1_MOUSE
ID Q99MM1_MOUSE PRELIMINARY; PRT; 413 AA.
AC Q99MM1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE WSL-1-like protein.
GN Name=Tnfrsf25;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=129/Sv;
RL MEDLINE=21158384; PubMed=11261933; DOI=10.1007/s002510000290;
RA Wang B.C.Y., Kitson J., Thern A., Williamson J., Farrow S.N.,
RA Owen M.J.;
RT "Genomic structure, expression, and chromosome mapping of the mouse
RT homologue for the WSL-1 (DR3, Apo3, TRAMP, LARD, TR3, TNFRSF12)
RT gene.";
RL Immunogenetics 53:59-63 (2001).
DR EMBL: AF329969; AA011256.1; -; mRNA.
DR HSP: P19438; ICH.
DR Ensembl: ENSMUSG00000024793; Mus musculus.
DR MGI: MGI:1934667; Tnfrsf25.
DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0016021; C:integral to membrane; TAS.
DR InterPro: IPR000488; Death.
DR InterPro: IPR011029; DEATH like.
DR InterPro: IPR006209; EGF like.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; Death; 1.
DR Pfam: PF00020; TNFR_c6; 1.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS00017; DEATH DOMAIN; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS00050; TNFR_NGFR_2; 1.
DR SQ SEQUENCE 413 AA; 44453 MW; 69F21B85D0DABABF CRC64;

Query Match 60.18; Score 1397; DB 2; Length 413;
Best Local Similarity 62.98; Pred. No. 1.1e-88;
Matches 270; Conservative 28; Mismatches 103; Indels 28; Gaps 7;

Qy 1 MEQRPRCAAVAAALLVLLGARAQGGTRSPRCAGDFHKKIGLFCRCGCP 52
Db 1 MEARLURGVVPLFLPLLLLLLLLLLGGQGG--MSGRCDCASESQKRYGPPCCRGCP 59

Qy 53 AGHYLKPCTPECGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCASVAD 112
Db 60 KGHYKAPCAEPCGNSCLPCPSDTFLTRDHFKTDCTRCQVDEALQVTLNCSAKSD 119

Qy 113 TRCGKPGFVEQVQSVSSPFYQCPCLDCGALHRTLLCSRRDTCGT---CLPGF 169
Db 120 THCGCQSGWCVDCSTVPCGKSSPFCVPCGATTPVH-----EAPTRPCLPGF 167

Qy 170 YEHGDGVCSPCTSTLGSCEPERCAAVCGWRQVQVQLLAGLVVPLLAGLTYTYRHCHW 229
Db 168 YIRGNDCTCTPTGSSVCPACTAVCGWQKQFVQVLLG---VAFLEGALICAYCRWQP 224

Qy 230 HKPLVTADAGMEALTPPPATHLSPLDSAHLLAPPDSSEKIC-TVOLVNSWTPGYPET 288
Db 230 HKPLVTADAGMEALTPPPATHLSPLDSAHLLAPPDSSEKIC-TVOLVNSWTPGYPET 288
```


Db 225 CKAVVTADTAGTEPLASPTQAHLSASDSTGKICTTQVLGVNNTPLGSLST 284
 QY 289 QEALCPQVTSWDQLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDMDAVPARRWK 348
 Db 285 QEVVCCQSQPMDQLPNRTLTGTPSLPSPAPPAGSFAAVLQPGPOLYDMDAVPARRWK 344
 QY 349 EFVRTLTGLREAEIEAVEVEIGRFRDQOQYEMLKRQOQPGAGLVAAALERMGLDGCVD 408
 Db 345 EFVRTLTGLREAEIEAVEVEICRFRDQOQYEMLKRQOQPGAGLVAAALERMGLDGCVD 404
 QY 409 LRSRLQGP 417
 Db 405 LRSRLQGP 413
 RESULT 6
 Q8VD70_MOUSE PRELIMINARY; PRT; 387 AA.
 AC Q8VD70;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Tnfrsf25 protein.
 GN Name=Tnfrsf25;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zerbahn B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udutin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Salivary gland;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC017526; AAH17526.1; -, mRNA.
 DR HSSP; P19438; 11CH.
 DR Ensembl; ENSMUSG00000024793; Mus musculus.
 DR MGI; MGI:1934667; Tnfrsf25.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR011029; DEATH like.
 DR InterPro; IPR001368; EGF like.
 DR Pfam; PF00531; Death; 1.
 DR Pfam; PF00020; TNFR_c6; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 2.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.

DR PROSITE; PS01186; EGF 2; UNKNOWN 1.
 DR PROSITE; PS00520; TNFR_NGFR_1; UNKNOWN 1.
 DR PROSITE; PS00502; TNFR_NGFR_2; 1.
 SQ SEQUENCE 387 AA; 41640 MW; F16644666BAD68D3 CRC64;
 Query Match 54.0%; Score 1255; DB 2; Length 387;
 Best Local Similarity 57.7%; Pred. No. 7,1e-79;
 Matches 248; Conservative 26; Mismatches 92; Indels 64; Gaps 6;
 QY 2 EQRPRGCAVAAA-----LLVLGARAQGGTRSPRCDCAGDFHKKIGLFC 48
 Db 8 ERSPPGAATPGSTARVLQPLFLPLLLLLLLGGGGGG--MSGRCDCASESQRYPFFCC 66
 QY 49 RGCPCAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECAQCACDQASQVALENC 108
 Db 67 RGCPRGHTYMKAFCAEPCGNSTCLPCFSDTFLTRDNHFKTDCTRCQVCDEALQVLENC 126
 QY 109 AVADTRCGCKPGWFEVCQVSCVSSSPFYCQPCDCLGALHRRHLLCSRDDTCGCLPG 168
 Db 127 AKSDTHCGCGSGWCDSTPCGKSPFCGATTPVH----- 166
 QY 169 FVEHGDGVCSTLTGSCPCERCAAVCGWRQWVQVLLAGLVVPLLLGATLTYYRHCV 228
 Db 167 -----EAPT-----PLFWQVLLG---VAFLLGAILCAVCRWQ 197
 QY 229 PHKPLVTADAGMEALTPPPATHLSPLDSATLLAPPDSSEKIC-TVQLVGNSTWTPGYE 287
 Db 198 PKAVVTADTAGTETLASPTQAHLSASDSTGKICTTQVLGVNNTPLGSLQ 257
 QY 288 TQALCPQVTSWDQLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDMDAVPARRW 347
 Db 258 TQEVVCCQSQPMDQLPNRTLTGTPSLPSPAPPAGSFAAVLQPGPOLYDMDAVPARRW 317
 QY 348 KEFVRTLTGLREAEIEAVEVEIGRFRDQOQYEMLKRQOQPGAGLVAAALERMGLDGCVE 407
 Db 318 KEFVRTLTGLREAEIEAVEVEICRFRDQOQYEMLKRQOQPGAGLVAAALERMGLDGCVE 377
 QY 408 DLRSRLQGP 417
 Db 378 DLRSRLQGP 387
 RESULT 7
 Q5T8X3_HUMAN PRELIMINARY; PRT; 253 AA.
 ID Q5T8X3;
 AC Q5T8X3;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Tumor necrosis factor receptor superfamily, member 25.
 GN Name=TNFRSF25; ORFNames=RP4-650H14.2-003;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Gluthero R.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL158217; CAI22157.1; -, Genomic DNA.
 DR Ensembl; ENSG00000171680; Homo sapiens.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; P:transmembrane receptor activity; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR008063; Fas_receptor.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 1.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 2.

DR PROSITE; PS01186; EGF_2; UNKNOWN 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 253 AA; 26934 MW; 4CD06775B6E9292 CRC64;

Query Match 50.1%; Score 1164; DB 2; Length 253;
Best Local Similarity 99.0%; Pred. No. 9.3e-73;
Matches 200; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEQRPRCAVAALLLVILGARAQGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
DB 1 MEQRPRCAVAALLLVILGARAQGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60

QY 61 CTPEPCGNSTCLVCPQDTFLAWENHNHSECAQCACDEQASQVALENCSSAVADTRCGCKPG 120
DB 61 CTPEPCGNSTCLVCPQDTFLAWENHNHSECAQCACDEQASQVALENCSSAVADTRCGCKPG 120

QY 121 WFVECVSQVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCGVSCP 180
DB 121 WFVECVSQVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCGVSCP 180

QY 181 TSTLGSCPCERCAAVCGWRQFW 202
DB 181 TSTLGSCPCERCAAVCGWRQSRW 202

RESULT 8
Q578X8_HUMAN
ID Q578X8_HUMAN PRELIMINARY; PRT; 215 AA.
AC Q578X8;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Tumor necrosis factor receptor superfamily, member 25 (Fragment).
GN Names=TNFRSF25; ORFNames=RP4-650H14.2-010;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Glithero R.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL158217; CAI22152.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
KW Receptor.
SQ SEQUENCE 277 AA; 29111 MW; 3D19F3B847BFC093 CRC64;

Query Match 45.4%; Score 1054; DB 2; Length 277;
Best Local Similarity 72.6%; Pred. No. 4.3e-65;
Matches 204; Conservative 5; Mismatches 32; Indels 40; Gaps 8;

QY 1 MEQRPRGCAVAALLLVILGARAQGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
DB 1 MEQRPRGCAVAALLLVILGARAQGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60

QY 61 CTPEPCGNSTCLVCPQDTFLAWENHNHSECAQCACDEQASQVALENCSSAVADTRCGCKPG 120
DB 61 CTPEPCGNSTCLVCPQDTFLAWENHNHSECAQCACDEQASQVALENCSSAVADTRCGCKPG 120

QY 121 WFVECVSQVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCGVSCP 180
DB 121 WFVECVSQVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCGVSCP 180

QY 181 T--STLGSCP-----ERCAAVCGWR--OMFWQVLLAGLVVPLLLGATLTY 222
DB 181 TTPPSLAGAPWGAQVAVPLSVAGRGVGVGLGRVGEIGWTE----GRRV--RRGATT-- 232
QY 223 TYRHCPWPKPL---VTADAGMEALTPPPA-----THLSPL 255
DB 233 -----QHPPAFAVSLGPGAPGWPGPPPAWGHGPDHLHPPL 267

RESULT 10
Q578X2_HUMAN
ID Q578X2_HUMAN PRELIMINARY; PRT; 178 AA.
AC Q578X2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Tumor necrosis factor receptor superfamily, member 25 (Fragment).
GN Names=TNFRSF25; ORFNames=RP4-650H14.2-006;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;

DR PROSITE; PS01186; EGF_2; UNKNOWN 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 253 AA; 26934 MW; 4CD06775B6E9292 CRC64;

Query Match 50.1%; Score 1164; DB 2; Length 253;
Best Local Similarity 99.0%; Pred. No. 9.3e-73;
Matches 200; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEQRPRCAVAALLLVILGARAQGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
DB 1 MEQRPRCAVAALLLVILGARAQGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60

QY 61 CTPEPCGNSTCLVCPQDTFLAWENHNHSECAQCACDEQASQVALENCSSAVADTRCGCKPG 120
DB 61 CTPEPCGNSTCLVCPQDTFLAWENHNHSECAQCACDEQASQVALENCSSAVADTRCGCKPG 120

QY 121 WFVECVSQVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCGVSCP 180
DB 121 WFVECVSQVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCGVSCP 180

QY 181 TSTLGSCPCERCAAVCGWRQFW 202
DB 181 TSTLGSCPCERCAAVCGWRQSRW 202

RESULT 8
Q578X8_HUMAN
ID Q578X8_HUMAN PRELIMINARY; PRT; 215 AA.
AC Q578X8;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Tumor necrosis factor receptor superfamily, member 25 (Fragment).
GN Names=TNFRSF25; ORFNames=RP4-650H14.2-010;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Glithero R.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL158217; CAI22152.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
KW Receptor.
SQ SEQUENCE 277 AA; 29111 MW; 3D19F3B847BFC093 CRC64;

Query Match 45.4%; Score 1054; DB 2; Length 277;
Best Local Similarity 72.6%; Pred. No. 4.3e-65;
Matches 204; Conservative 5; Mismatches 32; Indels 40; Gaps 8;

QY 1 MEQRPRGCAVAALLLVILGARAQGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
DB 1 MEQRPRGCAVAALLLVILGARAQGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60

QY 61 CTPEPCGNSTCLVCPQDTFLAWENHNHSECAQCACDEQASQVALENCSSAVADTRCGCKPG 120
DB 61 CTPEPCGNSTCLVCPQDTFLAWENHNHSECAQCACDEQASQVALENCSSAVADTRCGCKPG 120

QY 121 WFVECVSQVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCGVSCP 180
DB 121 WFVECVSQVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCGVSCP 180

QY 181 T--STLGSCP-----ERCAAVCGWR--OMFWQVLLAGLVVPLLLGATLTY 222
DB 181 TTPPSLAGAPWGAQVAVPLSVAGRGVGVGLGRVGEIGWTE----GRRV--RRGATT-- 232
QY 223 TYRHCPWPKPL---VTADAGMEALTPPPA-----THLSPL 255
DB 233 -----QHPPAFAVSLGPGAPGWPGPPPAWGHGPDHLHPPL 267

RESULT 10
Q578X2_HUMAN
ID Q578X2_HUMAN PRELIMINARY; PRT; 178 AA.
AC Q578X2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE Tumor necrosis factor receptor superfamily, member 25 (Fragment).
GN Names=TNFRSF25; ORFNames=RP4-650H14.2-006;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;

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RN NUCLEOTIDE SEQUENCE.
RA Glithero R.;
RL EMBL: AL158217; CAI22158.1; -: Genomic_DNA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0004888; F:transmembrane receptor activity; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR GO: GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR006209; EGF like.
DR InterPro: IPR008063; Fas_receptor.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 1.
DR PRINTS: PR01680; FASRECEPTOR.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS01186; EGF 2; UNKNOWN 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00652; TNFR_NGFR_2; 1.
KW Receptor.
FT NON TER
SQ SEQUENCE 178 AA; 19044 MW; 474686B96FBF19F4 CRC64;

Query Match 44.6%; Score 1036; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 4.8e-64;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RPRCAVAALLLVLLGARAQGGTRSPRCAGDFHKKIIGLFCRCGCPAGHYLKAPCTE 63
DB 1 RPRCAVAALLLVLLGARAQGGTRSPRCAGDFHKKIIGLFCRCGCPAGHYLKAPCTE 60
QY 64 PCGNSTCLVCPQDPTFLAWNHNNHSECAQCACDQASQVALENCASVADTRCGCKPGWF 123
DB 61 PCGNSTCLVCPQDPTFLAWNHNNHSECAQCACDQASQVALENCASVADTRCGCKPGWF 120
QY 124 ECQVSQCVSPPFCQCLDCGALHRRHTRLLCSRRDTCGTCLPGFHEHGGCVSCPT 181
DB 121 ECQVSQCVSPPFCQCLDCGALHRRHTRLLCSRRDTCGTCLPGFHEHGGCVSCPT 178

RESULT 11
TNRIA_PIG
ID TNRIA_PIG STANDARD; PRT; 461 AA.
AC PS0555;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE tumor necrosis factor receptor superfamily member 1A precursor (p60)
DE (TNF-R1) (TNF-R1) (p55).
GN Name=TNFRSF1A; Synonyms=TNFR1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sub.
OX NCBI_TaxID=9823;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RX MEDLINE=96011645; PubMed=7590278; DOI=10.1016/0378-1119(95)00423-4;
RA Suter B., Pauli U.H.;
RT "Cloning of the cDNA encoding the porcine p55 tumor necrosis factor
  receptor.";
RL Gene 163:263-266(1995).
CC -1- FUNCTION: Receptor for TNFSP2/TNF-alpha and homotrimeric
CC TNFRSF1/lymphotoxin-alpha. The adapter molecule FADD recruits
CC caspase-8 to the activated receptor. The resulting death-inducing
CC signaling complex (DISC) performs caspase-8 proteolytic activation
CC which initiates the subsequent cascade of caspases (aspartate-
CC specific cysteine proteases) mediating apoptosis (By similarity).
CC -1- SUBUNIT: Binding of TNF to the extracellular domain leads to
CC homotrimerization. The aggregated death domains provide a novel
CC molecular interface that interacts specifically with the death
CC domain of TRADD. Various TRADD-interacting proteins such as TRAFs,

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CC RIP and possibly FADD, are recruited to the complex by their
CC association with TRADD. This complex activates at least two
CC distinct signaling cascades, apoptosis and NF-kappa-B signaling.
CC Binds BAG4. Constitutively associated with TRPC4AP (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: Both the cytoplasmic membrane-proximal region and the C-
CC terminal region containing the death domain are involved in the
CC interaction with TRPC4AP (By similarity).
CC -1- SIMILARITY: Contains 1 death domain.
CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL: U19994; AAC48499.1; -: mRNA.
CC FIR: JC4302; JC4302.
CC HSP: P19438; IICH.
CC SMR: P50555; 362-447.
CC InterPro: IPR000488; Death.
CC InterPro: IPR011029; DEATH_like.
CC InterPro: IPR001368; TNFR_c6.
CC Pfam: PF00531; Death; 1.
CC Pfam: PF00020; TNFR_c6; 3.
CC SMART: SM00005; DEATH; 1.
CC SMART: SM00208; TNFR; 4.
CC PROSITE: PS00017; DEATH_DOMAIN; 1.
CC PROSITE: PS00652; TNFR_NGFR_1; 3.
CC PROSITE: PS00652; TNFR_NGFR_2; 2.
CC Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 461 Tumor necrosis factor receptor
FT TOPO_DOM 22 210 Extracellular (Potential).
FT TRANSMEM 211 233 Potential.
FT TOPO_DOM 234 461 Cytoplasmic (Potential).
FT REPEAT 43 82 TNFR-Cys 1.
FT REPEAT 83 125 TNFR-Cys 2.
FT REPEAT 126 166 TNFR-Cys 3.
FT REPEAT 167 195 TNFR-Cys 4.
FT DOMAIN 362 447 Death.
FT REGION 340 350 N-SMase activation domain (NSD).
FT CARBOHYD 54 54 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 86 86 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 151 151 N-linked (GlcNAc...) (Potential).
FT DISULFID 44 58 By similarity.
FT DISULFID 59 72 By similarity.
FT DISULFID 62 81 By similarity.
FT DISULFID 84 99 By similarity.
FT DISULFID 102 117 By similarity.
FT DISULFID 105 125 By similarity.
FT DISULFID 127 143 By similarity.
FT DISULFID 146 158 By similarity.
FT DISULFID 149 166 By similarity.
FT DISULFID 168 179 By similarity.
FT DISULFID 182 194 By similarity.
FT DISULFID 185 190 By similarity.
SQ SEQUENCE 461 AA; 50696 MW; CD72361EC60C9D43 CRC64;

Query Match 17.9%; Score 415; DB 1; Length 461;
Best Local Similarity 30.5%; Pred. No. 1.4e-20;
Matches 140; Conservative 44; Mismatches 20; Indels 74; Gaps 18;

QY 11 VAAALLLVLLGARAQGGTRSPR-----GTRSPR---CDCAGDFHKKIIGLFCRCGCPAGHYLKAPCT 62
DB 14 VLRALLVDVYVPGVHGLVLPDREKRESLCPGGKYSHPNRSICCTCKCHKGYLHNDCL 73
QY 63 EPCGNSTCLVCPQDPTFLAWNHNNHSECAQCACDQASQVALENCASVADTRCGCKPGWF 122

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Db 74 GPGLDTCRCNDNGTFTASEN-HLTQCLSCSKCRSEMSQVEISPTCTVDRDVTVCGRKN-- 130
Qy 123 VECQVSCVSSPPYQPCPLDCGALHRHRLIC-SRRDTCGTCLPGFYEHGDCVSCPT 181
Db 131 ---QYRWSETLQCLNCSLCP--NGTVQPLCKEKQDTTC-NCHSGFFLRDKECVSCVN 184
Qy 182 STLGCSPERCAAVCGWRQMP-----WQVLLAGLVVPLLLGATLTYTYRHCHPH-- 230
Db 185 CKNADCKNLCPATSETRNDQDTGTTVLLPLVIFGLCLAFFLVGLACRYQWRKPKLYS 244
Qy 231 -----KPLVTADAGMEALTPPPATHLSPLD--SAHTLAPPDSSEKICTV 274
Db 245 IICGKSTPVKEGEPEPLATAPSG-----PITTFSPISFSPSTTTTFSPVSPISPP 297
Qy 275 QLVGNSWT--PGVPETQCALCPQVWTSWDLPSPALGPAAPTLP-----ESPAG 323
Db 298 TPTPCDSNLIKVTSPKIEAPPQAG-----PILMPPPASTPVTPLPKWGGSAHSAHS 352
Qy 324 SPAMMLQPGP-QLYDVNDVDAVPARKWEFVRTGLREAEIEBAVEVEIGR-FRDOQYEMLR 381
Db 353 APAQLADADPATLYAVVDGVPPTWKFEFVRRLGLSEHEIERLELQNGRCLREAQYSMLAE 412
Qy 382 WRQ---QOPAGLVAVYALERMGLDGCVEDLRSRLQGP 417
Db 413 WRRRTSREATLELLGSLVLRMDLLGCLDIEEAL-RGP 450

RESULT 12

Q6QHF0 MOUSE PRELIMINARY; PRT; 440 AA.
ID Q6QHF0 AC Q6QHF0; 1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE TNF receptor superfamily, member 1A (Fragment).
GN Name=Tnfalfa;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6JTCO; TISSUE=Liver;
RA Saelens J., Wielockx B., Puimege L., Vandenabeele A., Libert C.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY541590; AAS48429.1; -; mRNA.
DR SMR; Q6QHF0; 35-191, 351-435.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0005031; F:tumor necrosis factor receptor activity; TAS.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; TAS.
DR GO; GO:0008219; F:cell death; TAS.
DR GO; GO:0007166; P:cell surface receptor linked signal transdu. .; IMP.
DR GO; GO:0006952; P:defense response; IMP.
DR GO; GO:0006954; P:inflammatory response; IMP.
DR GO; GO:0007242; P:intracellular signaling cascade; TAS.
DR GO; GO:0007515; P:lymph gland development; IMP.
DR GO; GO:0006933; P:prostaglandin metabolism; TAS.
DR InterPro; IPR000488; Death.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS0017; DEATH DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER 1 1

FT NON_TER 440 440
SQ SEQUENCE 440 AA; 48639 MW; D343ED449B260188 CRC64;
Query Match 17.5%; Score 406.5; DB 2; Length 440;
Best Local Similarity 27.2%; Pred. No. 5.1e-20;
Matches 127; Conservative 56; Mismatches 191; Indels 93; Gaps 18;
Qy 11 VAAALLLVLAGARQQGT-----RSPRCDACAGDPKHKIGLFCRCGCPAGHYLKA 59
Db 5 LSLVLLALLAGIHPSGVTGLVPSLGDREKEDSLCPQGYVHKKNSICCTCKHGTLYS 64
Qy 60 PCTEPCGNSCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCASVADTRCGCKP 119
Db 65 DCPSPGRDTCRECEKGTFTASQNYLR-QCLSKCTCRKEMSQVEISPCQADKDTVCCK- 122
Qy 120 GMFVEQVSCVSSPPYQPCPLDCGALHRHRLICSSRRDTCGTCLPGFYEHGDCVSC 179
Db 123 -----ENQFORLYSETHFQCVDSCSP--FNGTVTPCKETQNTVCNCHAGFLESECVPC 176
Qy 180 PTSTLGSCP--ERCAAVC-----GWRQMFVQVLLAGLVVPLLLGATLTYTY 224
Db 177 -----SHCKKNEECMKLCLPPPLANVTNPQDSCTAVLLPLVILLGLCLLSFISLMCRY 231
Qy 225 RHCWP-----HKPLVTADAGMEALTPPPATHLSPLD--SAHTL-----APPDSEK 270
Db 232 PRWRPEVYSIICRDPVPVKEKAGKPLTPAPSPAFSPGTFNPTLGFSTPGFSPVSTP 291
Qy 271 ICTVQLVGNSSW-----TPGY-PETQALC-----PQVWTSWDLPSPALGPAAP 314
Db 292 ISPI-FGSPSNHXMPPVSEVVPTQGDPLLYESLCFVPAFTSPVQKWD----- 338
Qy 315 TLPSPSPAGSPAMMLQPGPOLYDVNDVDAVPARKWEFVRTGLREAEIEBAVEVEIGR-FRD 373
Db 339 SAHPQRPVADLAI-----LYAVVDGVPARKWEFVRFGSLSEHEIERLEMQNGRCLRE 392
Qy 374 QQYEMLRWRQQQPA---GLGAVYALERMGLDGCVEDLRSRLQGP 417
Db 393 AQYSMLEAWRRTPRHEDTLEVVLVSKMLAGCLNILEAL-RNP 438
RESULT 13
Q6QHF2 MUSSP PRELIMINARY; PRT; 440 AA.
ID Q6QHF2 AC Q6QHF2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE TNF receptor superfamily, member 1A (Fragment).
GN Name=Tnfalfa;
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SPRET/EI; TISSUE=Liver;
RA Saelens J., Wielockx B., Puimege L., Vandenabeele A., Libert C.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY541588; AAS48427.1; -; mRNA.
DR SMR; Q6QHF2; 35-191, 351-435.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005515; P:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.

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DR PROSITE; PSS0017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PSS0050; TNFR_NGFR_2; 3.
DR Receptor.
FT NON_TER 1
FT NON_TER 440
SQ SEQUENCE 440 AA; 48688 MW; 10E7BD7D289E0143 CRC64;

Query Match 17.5%; Score 405.5; DB 2; Length 440;
Best Local Similarity 28.1%; Pred. No. 5.9e-20;
Matches 132; Conservative 56; Mismatches 184; Indels 97; Gaps 22;

QY 11 VAAALLLVLLGARAQG-----GTRSPR---CDCAGDFHKKIGLFCRCGCPAGHYLKA 59
DB 5 LSLVLLALLMGHPSGVTGLVPSLGNREKRDLSLCPQGYVHSKNSISCTCKCHKGYLVS 64
QY 60 PCTEPCGNSTCLVCPQDTFLAENHNHSECARQACDEQASQVALENCASVADTRCGCKP 119
DB 65 DCPSPGRDVTVCRCCKGTFTASQNYLR-QCLSKCTCKEMSQVEISPCQADKDTVCCK- 122
QY 120 GMFVECVQSCVSSPFYCPQCLDCCGALHRRHLLCSRRDTCGTCPLPGFYEHGDCVSC 179
DB 123 -----ENQFORHLSTHFQCVDCSPC---FNGVTVPCKETQNTVCTCHAGFFLRESECVPC 176
QY 180 PTSTLGSCLP-ERCAAVC-----GWRQMFVQVLLAGLVVPLLLGATLTYT 224
DB 177 -----SHCKKQECMKLCLPPPLANTVNPQDSGTAVLLPLVILLGLLCSFIFSLMCRY 231
QY 225 RH-----CWPKPLVTADAGMEALTPPPATHLSPLDSAHLL-----APPDSS 268
DB 232 PRWRSEVYSIICRDSVP-VKEKAG-KPLTPAPSPAFSPSTSGFNPTLGFSTPGFSPVSS 289
QY 269 EKICTVOLGNSW-----TPGY-PETQALC-----PQVWMSDQLPSRAGPAA 312
DB 290 TPISPI-FGPSNMFMPPVSEVPTQADPLLYESLCSVPAPTSVQKWD-----PA- 340
QY 313 APTLSPSPAGSPAMMLQPGPOLYDMDVAPARRWKEFVRTLGLREAEIEAVEVEIGR-F 371
DB 341 -----HFQRPNDALAI-----LYAVDGVPPARKWKEFMRFMGLSEHIERLEMQNGHCL 390
QY 372 RDOQYEMLRKWRQOQPA---GLGAVYAALERMGLDGCVEDLSRLQGRP 417
DB 391 REAQYMLEAWRRRTPRHEDTLEVVGLVLSKMNLTGLENILEAL-RNP 438

RESULT 14
Q6QHF1 MOUSE PRELIMINARY; PRT; 440 AA.
AC Q6QHF1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE TNF receptor superfamily, member 1A (Fragment).
GN Name=TNfrsfla;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DBA/2CrlBr; TISSUE=Liver;
RA Staelens J., Wielockx B., Pulmege L., Vandenabeele A., Libert C.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY541589; AAS48428.1; -; mRNA.
DR SRR; G6QHF1; 35-191, 351-435.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0005031; F:tumor necrosis factor receptor activity; TAS.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; TAS.
DR GO; GO:0008219; P:cell death; TAS.

DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; IMP.
DR GO; GO:0006952; P:defense response; IMP.
DR GO; GO:0006954; P:inflammatory response; IMP.
DR GO; GO:0007242; P:intracellular signaling cascade; TAS.
DR GO; GO:0007515; P:lymph gland development; IMP.
DR GO; GO:0006693; P:prostaglandin metabolism; TAS.
DR InterPro; IPR000488; Death.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS0017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
DR Receptor.
FT NON_TER 1
FT NON_TER 440
SQ SEQUENCE 440 AA; 48632 MW; 580A2D2E334612A3 CRC64;

Query Match 17.4%; Score 404.5; DB 2; Length 440;
Best Local Similarity 27.2%; Pred. No. 7e-20;
Matches 127; Conservative 56; Mismatches 191; Indels 93; Gaps 18;

QY 11 VAAALLLVLLGARAQGGT-----RSPRCDCAGDFHKKIGLFCRCGCPAGHYLKA 59
DB 5 LSLVLLALLMGHPSGVTGLVPSLGNREKRDLSLCPQGYVHSKNSISCTCKCHKGYLVS 64
QY 60 PCTEPCGNSTCLVCPQDTFLAENHNHSECARQACDEQASQVALENCASVADTRCGCKP 119
DB 65 DCPSPGRDVTVCRCCKGTFTASQNYLR-QCLSKCTCKEMSQVEISPCQADKDTVCCK- 122
QY 120 GMFVECVQSCVSSPFYCPQCLDCCGALHRRHLLCSRRDTCGTCPLPGFYEHGDCVSC 179
DB 123 -----ENQFORHLSTHFQCVDCSPC---FNGVTVPCKETQNTVCTCHAGFFLRESECVPC 176
QY 180 PTSTLGSCLP-ERCAAVC-----GWRQMFVQVLLAGLVVPLLLGATLTYT 224
DB 177 -----SHCKKQECMKLCLPPPLANTVNPQDSGTAVLLPLVILLGLLCSFIFSLMCRY 231
QY 225 RH-----CWPKPLVTADAGMEALTPPPATHLSPLDSAHLL-----APPDSEK 270
DB 232 PRWRSEVYSIICRDPVPVKEKAGKPLTPAPSPAFSPSTSGFNPTLGFSTPGFSPVSS 291
QY 271 ICTVOLGNSW-----TPGY-PETQALC-----PQVWMSDQLPSRAGPAA 314
DB 292 ISPI-FGPSNMFMPPVSEVPTQADPLLYESLCSVPAPTSVQKWD----- 338
QY 315 TLPSPSPAGSPAMMLQPGPOLYDMDVAPARRWKEFVRTLGLREAEIEAVEVEIGR-FRD 373
DB 339 SAHPQPDNADLAI-----LYAVDGVPPARKWKEFMRFMGLSEHIERLEMQNGRCLRE 392
QY 374 QQYEMLRKWRQOQPA---GLGAVYAALERMGLDGCVEDLSRLQGRP 417
DB 393 AQYMLEAWRRRTPRHEDTLEVVGLVLSKMNLTGLENILEAL-RNP 438

RESULT 15
TNRIA MOUSE
ID TNRIA MOUSE STANDARD; PRT; 454 AA.
AC P25118;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 1A precursor (p50)
DE (TNF-R1) (TNF-R1) (p55).
GN Name=TNfrsfla; Synonyms=TNfr-1, TNfr1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
```

OX NCBI_TaxID=10090;
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91187885; PubMed=1849278;
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H.,
 RA Chen E.Y., Goeddel D.V.;
 RT "Cloning and expression of cDNAs for two distinct murine tumor
 RT necrosis factor receptors demonstrate one receptor is species
 RT specific.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834 (1991).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91246168; PubMed=1645445;
 RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
 RA Copeland N.G., Jenkins N.A., Smith C.A.;
 RT "Molecular cloning and expression of the type 1 and type 2 murine
 RT receptors for tumor necrosis factor.";
 RL Mol. Cell. Biol. 11:3020-3026 (1991).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91285014; PubMed=1647956;
 RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissonerghis A.M.,
 RA Gray P.W., Feldmann M., Foxwell B.M.J.;
 RT "Cloning, expression and cross-linking analysis of the murine p55
 RT tumor necrosis factor receptor.";
 RL Eur. J. Immunol. 21:1649-1656 (1991).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92039815; PubMed=1657766; DOI=10.1007/BF00211997;
 RA Roche J.G., Brockhaus M., Gentz R., Lesslauer W.;
 RT "Molecular cloning and expression of the mouse Tnf receptor type b.";
 RL Immunogenetics 34:338-340 (1991).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=94245292; PubMed=8188324; DOI=10.1007/BF00176168;
 RA Bebo B.F., Linthicum D.S.;
 RT "Nucleotide sequence of the TNF type I receptor from a mouse
 RT endothelioma cell line.";
 RL Immunogenetics 39:450-451 (1994).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=93156721; PubMed=8381516; DOI=10.1016/0161-5890(93)90088-S;
 RA Roche J., Bluthmann H., Gentz R., Lesslauer W., Steinmetz M.;
 RT "Genomic organization and promoter function of the murine tumor
 RT necrosis factor receptor beta gene.";
 RL Mol. Immunol. 30:165-175 (1993).
 RN [7]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C3H/He; TISSUE=Mesenchyme;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric
 CC TNFSF1/lymphotoxin-alpha. The adapter molecule FADD recruits

caspase-8 to the activated receptor. The resulting death-inducing
 signaling complex (DISC) performs caspase-8 proteolytic activation
 which initiates the subsequent cascade of caspases (aspartate-
 specific cysteine proteases) mediating apoptosis (By similarity).
 -1- SUBUNIT: Binding of TNF to the extracellular domain leads to
 homotrimerization. The aggregated death domains provide a novel
 molecular interface that interacts specifically with the death
 domain of TRADD. Various TRADD-interacting proteins such as TRAFs,
 RIP and possibly FADD, are recruited to the complex by their
 association with TRADD. This complex activates at least two
 distinct signaling cascades, apoptosis and NF-kappa-B signaling.
 Binds BAG4 (By similarity). Constitutively associated with
 TRPC4AP.
 -1- SUBCELLULAR LOCATION: Type I membrane protein.
 -1- DOMAIN: Both the cytoplasmic membrane-proximal region and the C-
 terminal region containing the death domain are involved in the
 interaction with TRPC4AP.
 -1- SIMILARITY: Contains 1 death domain.
 -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 EMBL: M60468; AAA39751.1; -; mRNA.
 EMBL: M59377; AAA40464.1; -; mRNA.
 EMBL: X59238; CAA41922.1; -; mRNA.
 EMBL: X57796; CAA40936.1; -; mRNA.
 EMBL: L26349; AAA59361.1; -; mRNA.
 EMBL: M76656; AAA40465.1; -; Genomic DNA.
 EMBL: M83067; AAA40465.1; JOINED; Genomic DNA.
 EMBL: M76655; AAA40465.1; JOINED; Genomic DNA.
 EMBL: BC004599; AAH04599.1; -; mRNA.
 EMBL: BC052675; AAH52675.1; -; mRNA.
 HSPR: P19438; IICH.
 PIR: A38634; GQMSIT.
 SMR: P25118; 41-197, 357-441.
 IntAct: P25118; -
 Ensembl: ENSMUSG0000030341; Mus musculus.
 MGI: MGI:1314884; Thirifila.
 GO: GO:0005615; C:extracellular space; TAS.
 GO: GO:0016021; C:integral to membrane; TAS.
 GO: GO:0005886; C:plasma membrane; TAS.
 GO: GO:0005031; F:tumor necrosis factor receptor activity; TAS.
 GO: GO:0005164; F:tumor necrosis factor receptor binding; TAS.
 GO: GO:0008219; P:cell death; TAS.
 GO: GO:0007166; P:cell surface receptor linked signal transdu. .; IMP.
 GO: GO:0006952; P:defense response; IMP.
 GO: GO:0006954; P:inflammatory response; IMP.
 GO: GO:0007242; P:intracellular signaling cascade; TAS.
 GO: GO:0007515; P:lymph gland development; IMP.
 GO: GO:0006693; P:prostaglandin metabolism; TAS.
 InterPro: IPR000488; Death.
 InterPro: IPR011029; DEATH like.
 InterPro: IPR001368; TNFR_C6.
 Pfam: PF00531; Death; 1.
 Pfam: PF00020; TNFR_C6; 3.
 PROSITE: PS00017; DEATH DOMAIN; 1.
 PROSITE: PS00652; TNFR_NGFR_1; 3.
 PROSITE: PS00050; TNFR_NGFR_2; 3.
 Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
 SIGNAL 1 21 Potential.
 CHAIN 22 454 Tumor necrosis factor receptor
 superfamily member 1A.
 TOPO_DOM 22 212 Extracellular (Potential).
 TRANSMEM 213 235 Potential.
 TOPO_DOM 236 454 Cytoplasmic (Potential).
 REPEAT 43 82 TNFR-Cys 1.
 REPEAT 83 125 TNFR-Cys 2.
 REPEAT 126 166 TNFR-Cys 3.
 REPEAT 167 196 TNFR-Cys 4.

```
FT DOMAIN 356 441 Death.
FT REGION 339 349 N-Sase activation domain (NSD).
FT CARBOHYD 54 54 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 151 151 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 202 202 N-linked (GlcNAc...) (Potential).
FT DISULFID 44 58 By similarity.
FT DISULFID 59 72 By similarity.
FT DISULFID 62 81 By similarity.
FT DISULFID 84 99 By similarity.
FT DISULFID 102 117 By similarity.
FT DISULFID 105 125 By similarity.
FT DISULFID 127 143 By similarity.
FT DISULFID 146 158 By similarity.
FT DISULFID 149 166 By similarity.
FT DISULFID 168 179 By similarity.
FT DISULFID 182 195 By similarity.
FT DISULFID 185 191 By similarity.
FT CONFLICT 394 394 R -> G (in Ref. 6).
SQ SEQUENCE 454 AA; 50130 MW; 0710C2E8C3C2B6D9 CRC64;

Query Match 17.4%; Score 404.5; DB 1; Length 454;
Best Local Similarity 27.2%; Pred. No. 7.2e-20;
Matches 127; Conservative 56; Mismatches 191; Indels 93; Gaps 18;

QY 11 VAAALLVILGARAQGT-----RSRCDACAGDFHKXIGLFCRCRGPAGHYLKA 59
Db 11 LSLVLLALLGIHPSGVTGLVPSLGDREKDSLCPQGYVHSKNNISICTKCHKGYLVS 70

QY 60 PCTEPCGNSTCLVCPQDTFLAWNHNSRCARQACDEQASQVALENCNSAVADTRCGCKP 119
Db 71 DCPSPGDRDTCRECEKGTFTASQNYLR-QCLSKCTCRKMSQVEISPCQADKDTVCCK- 128

QY 120 GWFVECVQSCVSSPFYCPCLDCGALHRRHRLLCRRDTCGTCPLPGFYEHGDCVCSC 179
Db 129 -----ENQFQRYLSETHPQCVCSPC--FNGTVIPCKETQNTVCNCHAGFFLESECVPC 182

QY 180 PTSTLGSCP--ERCAAVC-----GWRQMFVQVQVLLAGLVVPLLLGATLITY 224
Db 183 -----SHCKKNECMKLCPLPLANVTNPQDSGTAVLLPLVILLGLLSFIFISLMCRY 237

QY 225 RHCWP-----HKPLVTADAGHEALTPPPATHLSPLDSAHTLL-----APPDSEK 270
Db 238 PRWRPEVYSIICRDPVPVKEEKAGKPLTPAPSPAFSPTSGFNPTLGFSTFGFSFVSSTP 297

QY 271 ICTVQLVGNW-----TPGY-PETOEALC----PQVTSWDOLPSRALGPAAAP 314
Db 298 ISPI-FGPSNWHFMPVSEVVTQGADPLLYESLCSVPAPTSVQKWD----- 344

QY 315 TLPSPSPAGSPAMLPQPOLYDMDAVPARRWKEFVRTILGLREAEIETAEVEIGR-FRD 373
Db 345 SAHPQRPDNLAI-----LYAVVDGVPPARWKEFMRFMGLSEHEIERLEMONGRCIRE 398

QY 374 QQYEMLKRWQQQPA-----GLGAVYAALERMGLDGVEDLRSRLQRP 417
Db 399 AQYSMLAEWRRTPRHEDTLEVVGLVLSKNVLAGCLNILEAL-RNP 444
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Search completed: March 20, 2006, 08:01:09
Job time : 111 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 07:59:04 ; Search time 86 Seconds
(without alignments)
2130.476 Million cell updates/sec

Title: US-10-081-280-6

Perfect score: 2323

Sequence: 1 MEQPRGCAAAVAAALLLVLL.....ERMGLDGCVEDLRSRLQRGP 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2323	100.0	417	2	Aaw31517 Death dom
2	2323	100.0	417	2	Aaw26709 Human apo
3	2323	100.0	417	2	Aaw57045 Human apo
4	2323	100.0	417	2	Aaw95538 Death dom
5	2323	100.0	417	2	Aay05743 Tumour ne
6	2323	100.0	417	3	Aab36265 Human dea
7	2323	100.0	417	4	Aab97370 Human rhe
8	2323	100.0	417	5	Aao17879 Human rhe
9	2323	100.0	417	5	Aau86139 Human PRO
10	2323	100.0	417	6	Abg73993 Human Apo
11	2323	100.0	417	6	Abu08252 Human Apo
12	2323	100.0	417	6	Abg73859 Human foe
13	2323	100.0	417	6	Abu10204 Human GEN
14	2323	100.0	417	6	Ada00738 Human GEN
15	2323	100.0	417	6	Abg73824 Human apo
16	2323	100.0	417	6	Ada49692 Human Apo
17	2323	100.0	417	7	Abw02265 Human TNF
18	2323	100.0	417	7	Adg88381 Human dea
19	2323	100.0	417	7	Adj37305 Human tum
20	2323	100.0	417	7	Adn58869 Human BEC
21	2323	100.0	417	8	Adh34623 TNF recep
22	2323	100.0	417	8	Adg68229 Human PRO
23	2323	100.0	417	8	Adl27893 Human Dea
24	2323	100.0	417	8	Adq16568 Human dea

ALIGNMENTS

RESULT 1

AAW31517

ID AAW31517 standard; protein; 417 AA.

XX

AC AAW31517;

XX

DT 02-MAR-1998 (first entry)

XX

DE Death domain containing receptor DR3.

XX

KW Death domain containing receptor; DR3-V1; human; apoptosis; inflammation;

KW NF-kappaB.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

FT Domain

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Adq59120 Human dea
Adu04624 Tumour ne
Aab4941 Amino aci
Adh50948 Human dea
Aaw4486 Human DR3
Abg73995 Human Apo
Abg73862 Human foe
Adl15011 Human WSL
Abm84914 Human dia
Abm84915 Human dia
Aaw31516 Death dom
Aaw95537 Death dom
Aab36264 Human dea
Adg88379 Human DR3
Adl27891 Human dea
Ady17600 PRO polyp
Aab01337 TNF recep
Aab50918 Human PRO
Aaw57046 Mouse apo
Adl15009 Human WSL
Adl15010 Human WSL

25 2323 100.0 417 8 ADQ59120
26 2323 100.0 417 8 Adu04624
27 2323 100.0 418 4 Aab4941
28 2323 100.0 418 8 Adh50948
29 2323 100.0 833 6 Aaw4486
30 2308.5 99.4 416 6 Abg73995
31 2308.5 99.4 416 6 Abg73862
32 2306 99.3 417 7 Adl15011
33 2292 98.7 451 8 Abm84914
34 2277.5 98.0 450 8 Abm84915
35 2267 97.6 428 2 Aaw31516
36 2267 97.6 428 2 Aaw95537
37 2267 97.6 428 3 Aab36264
38 2267 97.6 428 8 Adg88379
39 2267 97.6 428 8 Adl27891
40 2196.5 94.6 426 9 Ady17600
41 2179.5 93.8 426 3 Aab01337
42 1862 80.2 343 4 Aab50918
43 1404 60.4 411 2 Aaw57046
44 1164 50.1 253 7 Adl15009
45 1052.5 45.3 218 7 Adl15010

Location/Qualifiers
1..24
/label= Sig_peptide
25..201
/note= "extracellular domain"
202..224
/note= "transmembrane domain"
225..417
/note= "intracellular domain"
342..408
/note= "death domain"

WO9733904-A1.
18-SEP-1997.
17-OCT-1996; 96WO-US016849.
12-MAR-1996; 96US-0013285P.
(HUMA-) HUMAN GENOME SCI INC.
(UNMI) UNIV MICHIGAN.
Yu G, Ni J, Dixit VM, Gentz RL, Dillon PJ;
WPI; 1997-470812/43.
N-PSDB; AAT89427.

Death domain containing receptor polypeptide(s) DR3 and DR3-V2 - for
activation of apoptosis and NF-kappaB, antagonists can be used to treat
inflammatory diseases.

Claim 1; Page 75-77; 108pp; English.

This protein comprises human death domain containing receptor DR3, a novel member of the tumour necrosis factor receptor family. Its amino acid sequence was deduced from a cDNA clone (see AAT89427) isolated from a HUVBC cDNA library. Related death domain containing receptor DR3-V1 (see AAW31516) has also been identified. Recombinant full-length or mature DR3, or the extracellular, transmembrane, intracellular or death domain of DR3 can be expressed in transformed host cells. These polypeptides can be used to treat diseases and disorders associated with the inhibition of apoptosis, or to screen for modulator compounds. Antagonists, such as antibodies raised against DR3-V1, can be used to treat diseases and disorders associated with increased apoptosis and for treating inflammatory diseases and disorders

Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKI GLFCCRCGPAGHYLKAP 60
DB 1 MEQRPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKI GLFCCRCGPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAQCACDEQASQVALENCSSAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAQCACDEQASQVALENCSSAVADTRCGCKPG 120
QY 121 WFVEQCVSQCVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCVSCP 180
DB 121 WFVEQCVSQCVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCVSCP 180
QY 181 TSTLGSCEPCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTRHCWPHKPLVTAD 240
DB 181 TSTLGSCEPCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTRHCWPHKPLVTAD 240
QY 241 MEALTPPPATHLSPDLSAHTLLAPDSSSEKI CTQVLVGNVSWTPGYETQALCPQVTWSW 300
DB 241 MEALTPPPATHLSPDLSAHTLLAPDSSSEKI CTQVLVGNVSWTPGYETQALCPQVTWSW 300

RESULT 2

AAW26709
ID AAW26709 standard; protein; 417 AA.

XX AAW26709;
AC AAW26709;
XX AAW26709;
DT 14-APR-1998 (first entry)
XX Human apoptosis protein Apo-3.
DE Apo-3; apoptosis; human; therapy.
XX Homo sapiens.
OS Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..24
FT /label= Sig_peptide
FT Domain 25..198
FT /note= "extracellular domain"
FT Modified-site 67
FT /note= "N-glycosylated"
FT Modified-site 106
FT /note= "N-glycosylated"

FT Domain 199..224
FT /note= "transmembrane domain"
FT Domain 225..417
FT /note= "intracellular domain"
FT Domain 338..417
FT /note= "death domain"

PN WC9737020-A1.
XX 09-OCT-1997.
XX 31-MAR-1997; 97WO-US005230.
XX 01-APR-1996; 96US-00625328.
XX 23-SEP-1996; 96US-00710802.
XX (GETH) GENENTECH INC.

XX Ashkenazi AJ;
XX WPI; 1997-503105/46.
XX N-PSDB; AAT91180.

Polypeptide(s) Apo-3 and Apo-2LI - useful for regulating apoptosis in mammalian cells.

Claim 19; Page 46-48; 70pp; English.

This novel polypeptide, designated Apo-3, is a protein that stimulates or induces apoptotic activity in mammalian cells purposes. Its amino acid sequence was deduced from a human foetal heart cDNA clone (see AAT91180). The N-terminal 181 amino acids of Apo-3 are identical to the sequence of another novel apoptosis polypeptide, Apo-2LI (see AAW26709). Also claimed are: polypeptides comprising the extracellular or death domain of Apo-3; chimeric molecules comprising Apo-3 fused to a heterologous amino acid sequence; antibodies that bind to Apo-3 or its extracellular domain; nucleic acids encoding the polypeptides, as well as vectors and host cells; a non-human transgenic animal containing cells that express nucleic acid encoding Apo-3; and a non-human knockout animal containing cells having an altered Apo-3 gene. Apo-3 can be used to induce apoptosis or NF-kappa-B- (NF-kB)- or JNK-mediated gene expression for therapeutic purposes. Apo-3-IgG fusion proteins can be used to inhibit apoptosis or NF-kB activation or JNK activation for therapeutic purposes, and can be used as immunogens for anti-Apo-3- antibody production. Apo-3 or Apo-2LI can also be used as assay standards. The animals can be used in drug screening and development

Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQRPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKI GLFCCRCGPAGHYLKAP 60
DB 1 MEQRPRGCAVAALLLVLLGARAQGGTSPRCDCAGDFHKKI GLFCCRCGPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAQCACDEQASQVALENCSSAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAQCACDEQASQVALENCSSAVADTRCGCKPG 120
QY 121 WFVEQCVSQCVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCVSCP 180
DB 121 WFVEQCVSQCVSSSPFYCPCLDCGALHRRHTRLLCSRRDTCGTCLPGFYEHGDCVSCP 180
QY 181 TSTLGSCEPCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTRHCWPHKPLVTAD 240
DB 181 TSTLGSCEPCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTRHCWPHKPLVTAD 240
QY 241 MEALTPPPATHLSPDLSAHTLLAPDSSSEKI CTQVLVGNVSWTPGYETQALCPQVTWSW 300
DB 241 MEALTPPPATHLSPDLSAHTLLAPDSSSEKI CTQVLVGNVSWTPGYETQALCPQVTWSW 300

QY 301 DQLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDMDVAVPARWKKEFVRTLGLEAE 360
DB 301 DQLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDMDVAVPARWKKEFVRTLGLEAE 360
QY 361 IEAVEVEIGFRDQOQYEMLKRWQOQPGAGLGAVYAALERMGLDGCVEDLRSRLQGP 417
DB 361 IEAVEVEIGFRDQOQYEMLKRWQOQPGAGLGAVYAALERMGLDGCVEDLRSRLQGP 417

RESULT 3
AAW57045
ID AAW57045 standard; protein; 417 AA.
XX
AC AAW57045;
DT 20-AUG-1998 (first entry)
XX Human apoptosis inducing receptor.
DE
XX
KW Apoptosis inducing receptor; AIR protein; human; cell death regulator;
KW Type I transmembrane protein; tumour cell death; autoimmune disease;
KW therapy.
XX
OS Homo sapiens.
XX
PN WO9814565-A1.
XX
PD 09-APR-1998.
XX
PF 03-OCT-1997; 97WO-US017876.
XX
PR 04-OCT-1996; 96US-0044456P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Perkins PA;
XX
DR WPI; 1998-240077/21.
DR N-PSDB; AAV28700.
XX
PT DNA encoding apoptosis inducing receptor - which is Type I transmembrane
PT protein, useful for regulating cell death.
XX
PS Claim 16; Page 28-30; 45pp; English.
XX
CC This sequence is the human apoptosis inducing receptor (AIR) of the
CC invention. AIR is a Type I transmembrane protein, soluble forms of which
CC can be used to regulate cell death in a therapeutic setting. Soluble AIR
CC can also be used in vitro to block apoptosis or AIR-expressing cells, or
CC to screen agonists or antagonists of AIR activity. The cytoplasmic domain
CC of AIR can be used to develop assays for inhibitors of AIR-induced cell
CC death, which is useful to regulate cell death in a therapeutic setting as
CC well as in vitro. Agonists of AIR activity can be used to kill tumour
CC cells that express AIR, or T cells expressing AIR in autoimmune diseases
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAVAALLLVLLGARAQGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
DB 1 MEQPRGCAVAALLLVLLGARAQGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
QY 61 CTPECGNSTCLVCPQDTFLAWENHNHSECAQACDEQASQVALENCNSAVADTRCGCKPG 120
DB 61 CTPECGNSTCLVCPQDTFLAWENHNHSECAQACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVECVQSCVSSPFCVCPCLDGCALHRRHTRLLCSRRDTCCTCLPGFVEHGDGVSCP 180
DB 121 WFVECVQSCVSSPFCVCPCLDGCALHRRHTRLLCSRRDTCCTCLPGFVEHGDGVSCP 180

QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYYRHCHWPKPLVLTADAG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYYRHCHWPKPLVLTADAG 240
QY 241 MEALTPPPATHLSPLDSANTLAPPDSSEKICTVQLVGNHSWTGYPETQEQALCPQVTWSW 300
DB 241 MEALTPPPATHLSPLDSANTLAPPDSSEKICTVQLVGNHSWTGYPETQEQALCPQVTWSW 300
QY 301 DQLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDMDVAVPARWKKEFVRTLGLEAE 360
DB 301 DQLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDMDVAVPARWKKEFVRTLGLEAE 360
QY 361 IEAVEVEIGFRDQOQYEMLKRWQOQPGAGLGAVYAALERMGLDGCVEDLRSRLQGP 417
DB 361 IEAVEVEIGFRDQOQYEMLKRWQOQPGAGLGAVYAALERMGLDGCVEDLRSRLQGP 417

RESULT 4
AAW95538
ID AAW95538 standard; protein; 417 AA.
XX
AC AAW95538;
DT 25-MAR-1999 (first entry)
XX
DE Death domain containing receptor polypeptide (DR3).
XX
KW Death domain; receptor; DR3-V1; DR3; recombinant.
XX
OS Homo sapiens.
XX
FH Key
FT Peptide 1..24
FT Protein /note= "signal peptide"
FT /note= "mature protein"
XX
PN JP11000170-A.
XX
PD 06-JAN-1999.
XX
PF 12-MAR-1997; 97JP-00057503.
XX
PR 12-MAR-1996; 96US-0013285P.
PR 17-OCT-1996; 96US-0028711P.
PR 06-FEB-1997; 97US-0037341P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX (UNMI) UNIV MICHIGAN.
XX
DR WPI; 1999-124390/11.
DR N-PSDB; AAX00925.
XX
PT New death domain containing receptor and recombinant vector - optionally
PT comprising leader sequence.
XX
PS Claim 1; Fig 3; 50pp; Japanese.
XX
CC The invention provides nucleotide sequences encoding death domain
CC containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone is
CC contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
CC contained in ATCC deposition No. 97757. Recombinant vectors comprising
CC the nucleic acid sequences and optionally the leader sequences are used
CC for the recombinant production of the proteins. The present sequence
CC represents the amino acid sequence of a death domain containing receptor
CC polypeptide (DR3)
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
 DB 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
 QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAACQACDEQASQVALENCASAVADTRCGCKPG 120
 DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAACQACDEQASQVALENCASAVADTRCGCKPG 120
 QY 121 WFVECVQSVSSSPFYCQCLDCGALHRRHTRLLCSRRDTCGTC LCPGFYEHGDCVSCP 180
 DB 121 WFVECVQSVSSSPFYCQCLDCGALHRRHTRLLCSRRDTCGTC LCPGFYEHGDCVSCP 180
 QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYT YRHCWPKPLVTADG 240
 DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYT YRHCWPKPLVTADG 240
 QY 241 MEALTTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGN SMTGYPETQALCPQVTWSW 300
 DB 241 MEALTTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGN SMTGYPETQALCPQVTWSW 300
 QY 301 DQLPSRALGPAAPTLSPPSPAGSPAMMLQPGPOLYDVM DAVPARRWKEFVRTLGLEAE 360
 DB 301 DQLPSRALGPAAPTLSPPSPAGSPAMMLQPGPOLYDVM DAVPARRWKEFVRTLGLEAE 360
 QY 361 IEAVEVEIGRFRDQOQYEMLKRWQOQPGAGLVAVYAL ERMLDGCVEDLRSRLQGP 417
 DB 361 IEAVEVEIGRFRDQOQYEMLKRWQOQPGAGLVAVYAL ERMLDGCVEDLRSRLQGP 417

RESULT 5

AAV05743

ID AAV05743 standard; protein; 417 AA.

AC AAV05743;

XX

XX 19-JUL-1999 (first entry)

XX Tumour necrosis factor receptor TR3.

XX

XX Tumour necrosis factor receptor; TR3; DR3; Apo3; WSL-1; LARD; agonist;
 KW antagonist; screening; human; Alzheimer's disease; AIDS; cancer;
 KW inflammation; arthritis; septicemia; autoimmune disease; psoriasis;
 KW inflammatory bowel disease; transplant rejection;
 KW graft versus host disease; infection; stroke; ischaemia;
 KW acute respiratory disease syndrome; restenosis; brain injury;
 KW bone disease; atherosclerosis; therapy.

XX Homo sapiens.

XX

XX EP911633-A1.

XX

XX 28-APR-1999.

XX

XX 02-OCT-1998; 98EP-00203332.

XX

XX 08-OCT-1997; 97US-0061334P.

XX

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX

XX McDonnell PC, Young PR, Zou J;

XX

XX WPI; 1999-246560/21.

XX

XX Identifying agonists and antagonists of tumor necrosis factor related
 PT receptors TR1, TR3 and TR5, and of ligand TL3, useful for treatment of
 PT cancer, AIDS, Alzheimer's disease, bone disease etc.

XX

XX Disclosure; Page 12-13; 23pp; English.

XX

XX The present sequence represents tumour necrosis factor receptor (TNFR)
 CC TR31, also known as DR3, Apo3, WSL-1 or LARD. The invention relates to
 CC TNFR related polypeptides TR1, TR3 and TR5 (see AAY05742-44) and their
 CC ligand TL3 (see AAY05745). TR1, TR3, TR5 and TL3 are used in claimed

CC methods of identifying agonists and antagonists, i.e. compounds that bind
 CC to the receptors or ligand, and which activate (agonist) or inhibit
 CC activation of (antagonists) TR1, TR3, TR5 or TL3. A screening kit for
 CC identifying agonists, antagonists, ligands, receptors, substrates,
 CC enzymes etc. for TR1, TR3, TR5 or TL3 polypeptides is provided. The
 CC agonists and antagonists are useful for treatment of chronic and acute
 CC inflammation, arthritis, septicemia, autoimmune disease e.g.
 CC inflammatory bowel disease, psoriasis, transplant rejection, graft versus
 CC host disease, infection, stroke, ischaemia, acute respiratory disease
 CC syndrome, restenosis, brain injury, AIDS, bone diseases, cancer (e.g.
 CC lymphoproliferative disorders), atherosclerosis, Alzheimer's disease,
 CC etc., caused by imbalance of TR1, TR3, TR5 or TL3
 XX
 SQ Sequence 417 AA;

Query Match 100.0%; Score 2323; DB 2; Length 417;

Best Local Similarity 100.0%; Pred. No. 1.5e-161;

Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60

DB 1 MEQPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60

QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAACQACDEQASQVALENCASAVADTRCGCKPG 120

DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAACQACDEQASQVALENCASAVADTRCGCKPG 120

QY 121 WFVECVQSVSSSPFYCQCLDCGALHRRHTRLLCSRRDTCGTC LCPGFYEHGDCVSCP 180

DB 121 WFVECVQSVSSSPFYCQCLDCGALHRRHTRLLCSRRDTCGTC LCPGFYEHGDCVSCP 180

QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYT YRHCWPKPLVTADG 240

DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYT YRHCWPKPLVTADG 240

QY 241 MEALTTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGN SMTGYPETQALCPQVTWSW 300

DB 241 MEALTTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGN SMTGYPETQALCPQVTWSW 300

QY 301 DQLPSRALGPAAPTLSPPSPAGSPAMMLQPGPOLYDVM DAVPARRWKEFVRTLGLEAE 360

DB 301 DQLPSRALGPAAPTLSPPSPAGSPAMMLQPGPOLYDVM DAVPARRWKEFVRTLGLEAE 360

QY 361 IEAVEVEIGRFRDQOQYEMLKRWQOQPGAGLVAVYAL ERMLDGCVEDLRSRLQGP 417

DB 361 IEAVEVEIGRFRDQOQYEMLKRWQOQPGAGLVAVYAL ERMLDGCVEDLRSRLQGP 417

RESULT 6

AAB36265

ID AAB36265 standard; protein; 417 AA.

XX

XX AAB36265;

XX

XX 20-FEB-2001 (first entry)

XX

XX Human death domain containing receptor DR3.

XX

XX Human; death domain containing receptor; DR3; cancer;

XX autoimmune disorder; inflammation; cardiovascular disorder; infection;

XX neurodegenerative disease; angiogenesis.

XX

XX Homo sapiens.

XX

XX WO200064465-A1.

XX

XX 02-NOV-2000.

XX

XX 21-APR-2000; 2000WO-US010741.

XX

XX 22-APR-1999; 99US-0130488P.

XX

XX 28-MAY-1999; 99US-0136741P.

XX

PA	(HUMA-) HUMAN GENOME SCI INC.	XX	Rheumatoid arthritis; transmembrane protein; human.
PA	(UNMI) UNIV MICHIGAN.	KW	
PA	(YUGG/) YU G.	XX	
PA	(NLSJ/) NI J.	OS	Homo sapiens.
PA	(GENT/) GENTZ R L.	XX	
PA	(DILL/) DILLON P J.	PN	WO200132921-A2.
PA	(DIXI/) DIXIT V M.	XX	
XX		PD	10-MAY-2001.
PI	Yu G, Ni J, Gentz RL, Dillon PJ, Dixit VM;	XX	
XX		XX	01-NOV-2000; 2000WO-JP007690.
DR	WPI; 2000-687263/67.	PF	
DR	N-PSDB; AAC68777.	XX	
XX		PR	01-NOV-1999; 99JP-00310805.
XX	Treating graft-versus-host disease, cancer, immunodeficiency or an	XX	
PT	autoimmune disease comprising administering an antibody to Death Domain	PA	(SHIO/) SHIOZAWA S.
PT	Containing Receptor proteins and a second therapeutic agent.	XX	
XX		PI	Shiozawa S, Konishi Y;
XX		XX	
PS	Claim 1; Fig 2; 273pp; English.	DR	WPI; 2001-308750/32.
XX		DR	N-PSDB; AAH27782.
CC	The present invention provides the protein and coding sequences for two	XX	
CC	death domain containing receptors, designated DR3 and DR3-V1. These	XX	
CC	receptors are involved in apoptosis, and the sequences given can be used	PT	Diagnosing rheumatoid arthritis by probing digested human genomic DNA or
CC	in the treatment of cancers, infections, cardiovascular disorders such as	PT	comparing expression of mRNA or polypeptide of a region of transmembrane
CC	arrhythmias, ischaemia, aneurysms, arterial occlusive diseases, embolisms	XX	protein.
CC	and congenital heart defects, neurodegenerative diseases including	XX	
CC	Alzheimer's and Parkinson's diseases, autoimmune disease such as multiple	PS	Disclosure; Page 15-17; 21pp; Japanese.
CC	sclerosis, arthritis, diabetes, Graves' disease, asthma and psoriasis,	CC	
CC	and to promote angiogenesis and wound healing	CC	This invention relates to a method of diagnosing chronic rheumatoid
XX		CC	arthritis by digesting human genomic DNA with EcoRI and hybridising it
SQ	Sequence 417 AA;	CC	with a probe for the DNA encoding the present protein which is a
		CC	rheumatoid arthritis associated transmembrane protein. The method is used
		CC	for the diagnosis of chronic rheumatoid arthritis, and for developing new
		CC	treatments
		XX	
		SQ	Sequence 417 AA;
			Query Match 100.0%; Score 2323; DB 3; Length 417;
			Best Local Similarity 100.0%; Pred. No. 1.5e-161;
			Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MEQRPRGCAAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60		
Db	1 MEQRPRGCAAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60		
QY	61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG 120		
Db	61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG 120		
QY	121 WFEVCQVSCVSSSPFYCQPCLDGALHRRHTRLLCSRRTDCGTCLPGFYEHDGCVSCP 180		
Db	121 WFEVCQVSCVSSSPFYCQPCLDGALHRRHTRLLCSRRTDCGTCLPGFYEHDGCVSCP 180		
QY	181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTTADEAG 240		
Db	181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLLGATLTYTYRHCWPHKPLVTTADEAG 240		
QY	241 MEALTPPPATHLSPLDSAHTLLAPDSSEKI CTVOLVGNSTWTPGYETQALCPQVTSW 300		
Db	241 MEALTPPPATHLSPLDSAHTLLAPDSSEKI CTVOLVGNSTWTPGYETQALCPQVTSW 300		
QY	301 DQPSRALGPAAPATLSPSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLEAE 360		
Db	301 DQPSRALGPAAPATLSPSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLEAE 360		
QY	361 IEAVEVEIGFRDQOQYEMLKRWRQQQAGIGAVYAALERMGLDGCVEDLRSRLQRP 417		
Db	361 IEAVEVEIGFRDQOQYEMLKRWRQQQAGIGAVYAALERMGLDGCVEDLRSRLQRP 417		
			RESULT 8
			AA017879
			ID AA017879 standard; protein; 417 AA.
			XX
			AC AA017879;

XX DT 22-AUG-2002 (first entry)
 XX DE Human rheumatoid arthritis associated DR3 gene related protein #1.
 XX KW Human; DR3; rheumatoid arthritis; antirheumatic; antiarthritic;
 XX KW gene therapy.
 XX OS Homo sapiens.
 XX PN W0200234912-A1.
 XX PD 02-MAY-2002.
 XX PF 24-OCT-2001; 2001WO-JP009313.
 XX PR 24-OCT-2000; 2000JP-00324296.
 XX PR 27-MAR-2001; 2001JP-00090546.
 XX PR 30-MAR-2001; 2001JP-00099990.
 XX (NEWI-) NEW IND RES ORG.
 XX PA (SHIO/) SHIOZAWA S.
 XX PI Shiozawa S, Konishi Y;
 XX WPI; 2002-417132/44.
 XX DR N-PSDB; AAL47186.
 XX Genomes, particularly DR3 genomic DNA, participating in rheumatoid
 PT arthritis via mutation, useful in evaluating disease onset and its
 PT possibility and providing therapy and remedies.
 XX Claim 2; Page 69-70; 84pp; Japanese.
 XX The present invention relates to the human DR3 gene, which is associated
 CC with rheumatoid arthritis. Certain mutations in the gene can be linked to
 CC the disease. The sequences can be used to evaluate disease onset and its
 CC possibility and to provide therapy and remedies. The present sequence is
 CC a protein described in the exemplification of the invention
 XX Sequence 417 AA;
 XX
 Query Match 100.0%; Score 2323; DB 5; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.5e-161;
 Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEQPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKI GLFCRCPCPAGHYLKAP 60
 Db 1 MEQPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKI GLFCRCPCPAGHYLKAP 60
 QY 61 CTETPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCSSAVADTRCGCKPG 120
 Db 61 CTETPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCSSAVADTRCGCKPG 120
 QY 121 WFVEQCVQCVSSSPFYCQPCDCLGALHRRHTRLLCSRRDTCCTCLPGFYEHGDCGVSCP 180
 Db 121 WFVEQCVQCVSSSPFYCQPCDCLGALHRRHTRLLCSRRDTCCTCLPGFYEHGDCGVSCP 180
 QY 181 TSTLGSCTPCPCAAVCGWRQFWQVLLAGLVLPILLGATLTYTRHCWPHKPLVITADEAG 240
 Db 181 TSTLGSCTPCPCAAVCGWRQFWQVLLAGLVLPILLGATLTYTRHCWPHKPLVITADEAG 240
 QY 241 MEALTPTTATLSPDASHLLAPPDSSEKICTVQLVGNSTWTPGYETQALCPQVTWSW 300
 Db 241 MEALTPTTATLSPDASHLLAPPDSSEKICTVQLVGNSTWTPGYETQALCPQVTWSW 300
 QY 301 DQLPSRALGPAAATLSPESPAGSPAMMLQPGPOLYDVMQDAVPARWKEFVRLTGLREAE 360
 Db 301 DQLPSRALGPAAATLSPESPAGSPAMMLQPGPOLYDVMQDAVPARWKEFVRLTGLREAE 360
 QY 361 IEAVEVEIGFRQOQYEMLRWQOQPGAGLVAYVALERMLGDCGVEDLRSRLQRP 417
 Db 361 IEAVEVEIGFRQOQYEMLRWQOQPGAGLVAYVALERMLGDCGVEDLRSRLQRP 417

RESULT 9
 AAU86139
 ID AAU86139 standard; protein; 417 AA.
 XX AC AAU86139;
 XX 15-JUL-2002 (first entry)
 XX DE Human PRO779 polypeptide.
 XX KW Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
 KW leukaemia; neuronal disorder; stromal disorder; blastocoele disorder;
 KW inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;
 KW neuroprotective.
 XX OS Homo sapiens.
 XX PN W0200153486-A1.
 XX PD 26-JUL-2001.
 XX PF 11-FEB-2000; 2000WO-US003565.
 XX 08-MAR-1999; 99WO-US0005028.
 XX 11-MAR-1999; 99US-0123972P.
 XX 11-MAY-1999; 99US-0133459P.
 XX 02-JUN-1999; 99WO-US012252.
 XX 22-JUN-1999; 99US-0140650P.
 XX 22-JUN-1999; 99US-0140653P.
 XX 20-JUL-1999; 99US-0144758P.
 XX 26-JUL-1999; 99US-0145698P.
 XX 28-JUL-1999; 99US-0146222P.
 XX 17-AUG-1999; 99US-0149395P.
 XX 31-AUG-1999; 99US-0151689P.
 XX 01-SEP-1999; 99WO-US020111.
 XX 15-SEP-1999; 99WO-US021090.
 XX 30-NOV-1999; 99WO-US028313.
 XX 01-DEC-1999; 99WO-US028301.
 XX 01-DEC-1999; 99WO-US028634.
 XX 05-JAN-2000; 2000WO-US000219.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Goddard A, Godowski RJ, Gurney AL, Hillan KJ;
 PI Marschers SA, Pan J, Pitti RM, Roy NA, Smith V, Stone DM;
 PI Watanabe CK, Wood WI;
 XX WPI; 2002-205567/26.
 XX N-PSDB; ABK40265.
 XX Thirty five nucleic acids encoding PRO polypeptides, useful for treating
 PT benign or malignant tumors, leukemias and lymphoid malignancies,
 PT inflammatory, angiogenic and immunologic disorders.
 XX Claim 61; Fig 24; 302pp; English.
 XX The present invention relates to the isolation of novel human PRO
 CC polypeptides and the polynucleotide sequences encoding them. The PRO
 CC polypeptides, agonists, antagonists or anti-PRO antibodies are useful for
 CC treating benign or malignant tumours (e.g. renal, kidney, bladder,
 CC breast, etc), leukaemias and lymphoid malignancies, other disorders such
 CC as neuronal, glial, astrocytic, hypothalamic, glandular, macrophagal,
 CC stromal and blastocoele disorders, inflammatory, immune and angiogenic
 CC disorders. The polynucleotide sequences are also useful in gene therapy.
 CC AAU86128-AAU86162 represent the human PRO polypeptides of the invention
 XX Sequence 417 AA;
 XX
 Query Match 100.0%; Score 2323; DB 5; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.5e-161;
 Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MEQRPRGCAAAVALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQRPRGCAAAVALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVECOVSOVSSPPYCPCLDCGALHRRHRLTLLCSRRDTCGTCPLPGFYEHDGCVSCP 180
DB 121 WFVECOVSOVSSPPYCPCLDCGALHRRHRLTLLCSRRDTCGTCPLPGFYEHDGCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCWPHKPLVTADAEAG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCWPHKPLVTADAEAG 240
QY 241 MEALTPPPATHLSPLDSAHNTLLAPPDSSSEKICTVQLVGNSTPGYPETQALCPQVTWSW 300
DB 241 MEALTPPPATHLSPLDSAHNTLLAPPDSSSEKICTVQLVGNSTPGYPETQALCPQVTWSW 300
QY 301 DQLPSALGPAAAPTLSPEPSAGSPAMMLQPGPOLYDVMVDAVPARRWKEFVRTLGLREAE 360
DB 301 DQLPSALGPAAAPTLSPEPSAGSPAMMLQPGPOLYDVMVDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQOQYEMLKRWRQOQAGLGAVYAALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFRDQOQYEMLKRWRQOQAGLGAVYAALERMGLDGCVEDLRSRLQRP 417

RESULT 10
ABG73993
ID ABG73993 standard; protein; 417 AA.
AC ABG73993;
DT 01-APR-2003 (first entry)
XX Human Apo3 protein.
XX Apo-3; human; apoptosis; monoclonal antibody; cytostatic; cancer;
KW autoimmune; inflammatory; neurodegenerative disease.
XX Homo sapiens.
XX Key Location/Qualifiers
FT Peptide 1..24
FT Domain 25..198
FT Modified-site 67
FT Modified-site /note= "N glycosylated"
FT Domain 199..224
FT Domain /note= "Transmembrane domain"
FT Domain 225..417
FT Region /note= "Intracellular domain"
FT /note= "This Alanine is not present in the Apo3 variant
that is expressed in foetal heart"
XX US6469144-B1.
XX 22-OCT-2002.
XX 31-MAR-1997; 97US-00828683.
XX 01-APR-1996; 96US-00625328.
XX 23-SEP-1996; 96US-00710802.
XX (GETH ) GENENTECH INC.
XX
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PI Ashkenazi AJ;
XX WPI; 2003-147110/14.
DR N-PSDB; ABX15842.
XX
XX Novel isolated monoclonal antibody useful for activating or stimulating
PT apoptosis in cancer cells, comprises an antigen binding site which binds
PT to an Apo-2 ligand inhibitor polypeptide or to an Apo-3 polypeptide.
XX
PS Claim 1; Fig 4; 48pp; English.
XX
XX This invention relates to an isolated monoclonal antibody comprising an
CC antigen binding site which binds to an Apo-2 ligand inhibitor (Apo-2LI)
CC polypeptide and an antibody that binds the Apo3 protein. The antibodies
CC of the invention may have cytostatic activity and may act as activators
CC or stimulators of apoptosis in cancer cells, as blockers of excessive
CC apoptosis or of the autoimmune/inflammatory effects of Apo-3 resulting
CC from nuclear factor (NF)-kappaB activation or C-Jun-amino-terminal kinase
CC (JNK) activation. The anti-Apo-2 ligand inhibitor is useful in
CC therapeutic purposes for activating or stimulating apoptosis in cancer
CC cells and may be used to block excessive apoptosis (for example in
CC neurodegenerative disease), or to block potential autoimmune/
CC inflammatory effects of Apo-3 resulting from nuclear factor (NF)-kappaB
CC activation or C-Jun-amino-terminal kinase (JNK) activation. The antibody
CC may also be used in diagnostic assays for Apo-2LI or Apo-3, e.g.
CC detecting Apo-2LI or Apo-3 expression in specific cells, tissues or
CC serum, or for affinity purification of Apo-2LI or Apo-3 from recombinant
CC cell culture or natural sources. The present sequence represents the
CC human Apo3 protein which was used to generate the antibody of the
CC invention
XX
SQ Sequence 417 AA;
```

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Query Match 100.0%; Score 2323; DB 6; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEQRPRGCAAAVALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQRPRGCAAAVALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVECOVSOVSSPPYCPCLDCGALHRRHRLTLLCSRRDTCGTCPLPGFYEHDGCVSCP 180
DB 121 WFVECOVSOVSSPPYCPCLDCGALHRRHRLTLLCSRRDTCGTCPLPGFYEHDGCVSCP 180
QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCWPHKPLVTADAEAG 240
DB 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCWPHKPLVTADAEAG 240
QY 241 MEALTPPPATHLSPLDSAHNTLLAPPDSSSEKICTVQLVGNSTPGYPETQALCPQVTWSW 300
DB 241 MEALTPPPATHLSPLDSAHNTLLAPPDSSSEKICTVQLVGNSTPGYPETQALCPQVTWSW 300
QY 301 DQLPSALGPAAAPTLSPEPSAGSPAMMLQPGPOLYDVMVDAVPARRWKEFVRTLGLREAE 360
DB 301 DQLPSALGPAAAPTLSPEPSAGSPAMMLQPGPOLYDVMVDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQOQYEMLKRWRQOQAGLGAVYAALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFRDQOQYEMLKRWRQOQAGLGAVYAALERMGLDGCVEDLRSRLQRP 417
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RESULT 11
ABU08252
ID ABU08252 standard; protein; 417 AA.
XX ABU08252;
AC ABU08252;
XX
XX 13-MAY-2003 (first entry)
XX
```

XX DE Human Apo-3 protein.
 XX KW Human; Apo-2 ligand inhibitor; Apo-2LI; Apo-3; apoptosis; AIDS;
 KW acquired immunodeficiency syndrome; stroke; Alzheimer's disease; cancer;
 KW Parkinson's disease; amyotrophic lateral sclerosis; multiple sclerosis;
 KW retinitis pigmentosa; aplastic anaemia; cerebellar degeneration;
 KW myocardial infarction; reperfusion injury; toxin-induced liver disease;
 KW chromosome 1q36.3; programmed cell death.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Domain 1. .198
 FT /label= Extracellular domain
 FT /note= "This domain is claimed in claim 26"
 FT Domain 338. .417
 FT /label= Death domain
 FT /note= "This domain is claimed in claim 27"
 XX US2002165157-A1.
 XX 07-NOV-2002.
 XX 21-FEB-2002; 2002US-00081280.
 XX 01-APR-1996; 96US-0014699P.
 XX 23-SEP-1996; 96US-0026943P.
 XX 31-MAR-1997; 97US-00829270.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ;
 XX WPI; 2003-298703/29.
 XX N-PSDB; ABX13179.
 XX New biologically active Apo-2LI or Apo-3 polypeptide, useful for
 FT preparing a composition for treating cancer.
 XX Claim 22; Fig 4; 45pp; English.
 XX The invention relates to a new isolated biologically active Apo-2LI or
 CC Apo-3 having at least 80 % sequence identity with native sequence Apo-2LI or
 CC Apo-3 appearing as ABJ08251 and ABJ08252. Also included are a
 CC chimeric molecule comprising the Apo-2LI fused to a heterologous amino
 CC acid sequence; a dimer molecule comprising a first Apo-2LI and a second
 CC Apo-2LI; an antibody that binds to Apo-2LI or Apo-3 (or to its
 CC extracellular domain sequence); an isolated nucleic acid encoding Apo-2LI
 CC or Apo-3, a vector comprising the nucleic acid, a host cell comprising
 CC the vector, a method of producing Apo-2LI and a non-human (transgenic or
 CC knockout) animal that contains cells that express nucleic acid encoding
 CC Apo-3 or cells having an altered gene encoding Apo-3. Apo-2LI or Apo-3
 CC are involved in apoptosis (programmed cell death) which is implicated in
 CC AIDS, (acquired immunodeficiency syndrome), stroke, Alzheimer's disease,
 CC Parkinson's disease, amyotrophic lateral sclerosis, multiple sclerosis,
 CC retinitis pigmentosa, aplastic anaemia, cerebellar degeneration,
 CC myocardial infarction, reperfusion injury and toxin-induced liver
 CC disease. The gene for both proteins is located on chromosome 1q36.3 Apo-
 CC 2LI and Apo-3 are also useful for preparing a composition for treating
 CC cancer. The present sequence represents Apo-3
 XX Sequence 417 AA;
 XX Query Match 100.0%; Score 2323; DB 6; Length 417;
 XX Best Local Similarity 100.0%; Pred. No. 1.5e-161;
 XX Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEQPRGCAVAALLVLLGARAQGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
 DB 1 MEQPRGCAVAALLVLLGARAQGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
 QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAQCACDEQASQVALENCASAVADTRCGCKPG 120

Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECAQCACDEQASQVALENCASAVADTRCGCKPG 120
 QY 121 WFVECVQSVSSPFYQPCQCLDCGALHRRHRLLCSSRDTCGTCLPGFYEHGDCVSCP 180
 Db 121 WFVECVQSVSSPFYQPCQCLDCGALHRRHRLLCSSRDTCGTCLPGFYEHGDCVSCP 180
 QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTVRHCHWPKHPLVTADEAG 240
 Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTVRHCHWPKHPLVTADEAG 240
 QY 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWPGYPTQBALCPQVTSW 300
 Db 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWPGYPTQBALCPQVTSW 300
 QY 301 DQLPSRALGPAAPATLSPSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
 Db 301 DQLPSRALGPAAPATLSPSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
 QY 361 IEAVEVEIGRFRDQOYEMLRWQOQAPAGVYVALERMLGDCVEDLRSRLOGP 417
 Db 361 IEAVEVEIGRFRDQOYEMLRWQOQAPAGVYVALERMLGDCVEDLRSRLOGP 417
 XX RESULT 12
 XX ABG73859
 XX ID ABG73859 standard; protein; 417 AA.
 XX AC ABG73859;
 XX 03-APR-2003 (first entry)
 XX Human foetal heart Apo-3 protein.
 XX Human; Apo-3; apoptosis; induce apoptosis; inhibit apoptosis; TNFR;
 KW nuclear factor-kappa B; NF-kappa B; Alzheimer's disease; AIDS;
 KW tumour necrosis factor receptor; acquired immunodeficiency syndrome;
 KW Parkinson's disease; amyotrophic lateral sclerosis; multiple sclerosis;
 KW retinitis pigmentosa; cerebellar degeneration; aplastic anaemia;
 KW myocardial infarction; stroke; reperfusion injury;
 KW toxin-induced liver disease; cancer; lupus; herpes virus infection.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Domain 1. .198
 FT /note= "Extracellular domain. This domain is
 FT specifically claimed in claim 2 of the specification"
 FT Peptide 1. .24
 FT /label= Signal_peptide
 FT Protein 25. .417
 FT /note= "Mature Apo-3 protein"
 FT Modified-site 67
 FT /note= "N-glycosylated"
 FT Modified-site 106
 FT /note= "N-glycosylated"
 FT Domain 199. .224
 FT /note= "Transmembrane domain"
 FT Domain 225. .417
 FT /note= "Intracellular domain"
 FT Domain 338. .417
 FT /note= "Death domain. This domain is specifically
 FT claimed in claim 3 of the specification"
 XX US6462176-B1.
 XX 08-OCT-2002.
 XX 11-SEP-1997; 97US-00928069.
 XX 23-SEP-1996; 96US-0026943P.
 XX (GETH) GENENTECH INC.

XX Aahkenazi AJ;
PI WPI: 2003-173840/17.
DR N-PSDB; ABX15464.
XX Novel isolated Apo-3 polypeptide useful for inducing apoptosis in
PT mammalian cells, for generating antibodies, in affinity purification
PT techniques, and in competitive-type receptor binding assays.
XX Claim 1; Fig 8; 52pp; English.
XX The invention relates to an Apo-3 polypeptide having an extracellular
CC domain (ECD) sequence and a death domain sequence. The Apo-3 polypeptide
CC has been found to stimulate or induce apoptotic activity in mammalian
CC cells. Human Apo-3 exhibits similarities to the tumour necrosis factor
CC receptor (TNFR) family of polypeptides. The invention also relates to a
CC chimeric molecule comprising an extracellular domain sequence comprising
CC residues 1-198 of Apo-3 fused to a heterologous amino acid sequence. The
CC Apo-3 polypeptide is useful therapeutically to induce apoptosis in
CC mammalian cells. Decreased levels of apoptosis has been associated with
CC conditions such as cancer, lupus, and herpes virus infection. Increased
CC levels of apoptosis are associated with diseases such as acquired
CC immunodeficiency syndrome (AIDS), Alzheimer's disease, Parkinson's
CC disease, amyotrophic lateral sclerosis, multiple sclerosis, retinitis
CC pigmentosa, cerebellar degeneration, aplastic anaemia, myocardial
CC infarction, stroke, reperfusion injury, and toxin-induced liver disease.
CC The Apo-3 polypeptide is also useful in non-therapeutic applications such
CC as in quantitative diagnostic assays as a control against which samples
CC containing unknown quantities of Apo-3 may be prepared, in generating
CC antibodies, as standards in assays for Apo-3, in affinity purification
CC techniques, and in competitive-type receptor binding assays. The chimeric
CC molecule is useful therapeutically to inhibit apoptosis or nuclear factor
CC -kappa B (NF-kappa B) induction, or as an immunogen for producing anti-
CC Apo-3 antibodies. The present sequence represents the polypeptide
CC sequence of the human Apo-3 protein present in the foetal heart
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 2323; DB 6; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEQPRGCAAAVAAALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQPRGCAAAVAAALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTBPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCSSAVADTRCGCKPG 120
DB 61 CTBPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCSSAVADTRCGCKPG 120
QY 121 WFVECCQVSCVSSPFYQPCDCLGALHRRHTRLLCSRRDDCTCLPGFVEHGDGVSCP 180
DB 121 WFVECCQVSCVSSPFYQPCDCLGALHRRHTRLLCSRRDDCTCLPGFVEHGDGVSCP 180
QY 181 TSTLGSFCPCAAVCGWRQMFVQVLLAGLVVPLLGATLITYRHCHWPKPLVTADEAG 240
DB 181 TSTLGSFCPCAAVCGWRQMFVQVLLAGLVVPLLGATLITYRHCHWPKPLVTADEAG 240
QY 241 MEALTTPPPTHLSPLDSANTLLAPDSSEKICTVQLVGNSTWTPGYPETQALCPQVTSW 300
DB 241 MEALTTPPPTHLSPLDSANTLLAPDSSEKICTVQLVGNSTWTPGYPETQALCPQVTSW 300
QY 301 DQLPSRALGPAAPATLSPSPAGSPAMMLQPGPOLYDMDVAVPARWKEFVRTLGLREAE 360
DB 301 DQLPSRALGPAAPATLSPSPAGSPAMMLQPGPOLYDMDVAVPARWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGFRDQVQVEMLRWRQQQAGLGVAVYAALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGFRDQVQVEMLRWRQQQAGLGVAVYAALERMGLDGCVEDLRSRLQRP 417

RESULT 13

ABU10204
ID ABU10204 standard; protein; 417 AA.
XX
AC ABU10204;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human Apo-3.
XX
KW Human; Apo-3; apoptosis; gene therapy; inflammation; cancer;
KW neurodegenerative disease; immunosuppressive; tissue typing.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..24 /label= Signal_sequence
FT Protein 25..417 /label= Mature_Apo-3
FT Domain 25..198 /label= Extracellular_domain
FT Domain 199..224 /label= Transmembrane_domain
FT Domain 225..417 /label= Intracellular_domain
FT Domain 338..417 /label= Death_domain
XX
PN US2003004313-A1.
XX
PD 02-JAN-2003.
XX
PF 28-MAR-2002; 2002US-00112193.
XX
PR 23-SEP-1996; 96US-0026943P.
XX 11-SEP-1997; 97US-00928069.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ;
XX
DR WPI: 2003-438872/41.
DR N-PSDB; ACA61691.
XX
PT New isolated Apo-3 polypeptides, useful for stimulating or inducing
PT apoptotic activity in mammalian cells, e.g. cancer cells, or for in vivo
PT or ex vivo gene therapy techniques.
XX
PS Claim 5; Fig 8; 50pp; English.
XX
CC The invention relates to an isolated Apo-3 polypeptide. The Apo-3
CC polypeptides are useful for stimulating or inducing apoptotic activity in
CC mammalian cells e.g. cancer cells, or for in vivo or ex vivo gene therapy
CC techniques. The Apo-3 chimeric molecules are useful for inhibiting
CC apoptosis, or as immunogens used in generating antibodies. The
CC antagonistic antibodies may be used to block excessive apoptosis, for
CC instance in neurodegenerative disease, or to block potential autoimmune/
CC inflammatory effects of Apo-3 resulting from NF-kappaB activation. The
CC nucleic acid sequences are useful as diagnostics for tissue-specific
CC typing, for preparing Apo-3 polypeptides, or for generating transgenic or
CC knockout animals. The transgenic or knockout animals are useful in
CC developing and screening of therapeutically useful reagents. The present
CC sequence represents the amino acid sequence of human Apo-3
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 2323; DB 6; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEQPRGCAAAVAAALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQPRGCAAAVAAALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

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Db 61 CTBPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCSSAVADTRCGCKPG 120
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|
QY 121 WFVECVQSCVSSPPFYCPCLDCGALHRRHRLCSRRDTCGTCPLPGFYEHGDCVSCP 180
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Db 121 WFVECVQSCVSSPPFYCPCLDCGALHRRHRLCSRRDTCGTCPLPGFYEHGDCVSCP 180
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|
QY 181 TSTLGSCTPCERCAAVCGWRQFWQVLLAGLVLLIGATLTYTTRHCWPHKPLVTADDEAG 240
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Db 181 TSTLGSCTPCERCAAVCGWRQFWQVLLAGLVLLIGATLTYTTRHCWPHKPLVTADDEAG 240
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|
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QY 241 MEALTTPPPATHLSPLDSAHLLAPPDSSSEKICTVQLVGNSSWTPGYPETQALCPQVTWSW 300
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|
|
Db 241 MEALTTPPPATHLSPLDSAHLLAPPDSSSEKICTVQLVGNSSWTPGYPETQALCPQVTWSW 300
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|
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QY 301 DQLPSRALGPAAAPTLSPESSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
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Db 301 DQLPSRALGPAAAPTLSPESSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
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|
QY 361 IEAVEVEIGFRDQOYEMLRKRWQQQAGLGVAVYALERMGLDGCVEDLRSRLQGP 417
|
|
|
Db 361 IEAVEVEIGFRDQOYEMLRKRWQQQAGLGVAVYALERMGLDGCVEDLRSRLQGP 417
|
|
|
RESULT 14
ADA00738
ID ADA00738 standard; protein; 417 AA.
XX
AC ADA00738;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human GENCEPTIN protein SEQ ID NO:2.
XX
KW GENCEPTIN; obesity; lipid partitioning; lipid metabolism;
KW insulin-like activity; free fatty acid oxidation; weight reduction;
KW anorectic; antilipemic; antiarteriosclerotic; cardiant; antidiabetic;
KW hypotensive; ophthalmological; neuroprotective; nephrotropic;
KW obesity-related disease; insulin resistance; atherosclerosis;
KW atheromatous disease; heart disease; cardiac insufficiency;
KW coronary insufficiency; high blood pressure; hypertension; stroke;
KW syndrome X; diabetes mellitus; hyperlipidaemia; hyperuricaemia;
KW diabetic complication; microangiopathic lesion; ocular lesion;
KW retinopathy; neuropathy; renal lesion.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..24
FT Protein /label= signal
FT Domain 25..417
FT Region 25..199
FT Region /label= EC_domain
FT Region 34..71
FT Region /note= "Cys rich region"
FT Region 72..115
FT Region /note= "Cys rich region"
FT Misc-difference 97
FT Misc-difference /notes= "polymorphic amino acid Glu or Asp"
FT Misc-difference 98
FT Region /note= "polymorphic amino acid Gln or Glu"
FT Region 116..163
FT Region /note= "Cys rich region"
FT Region 164..192
FT Region /note= "Cys rich region"
FT Misc-difference 167
FT Domain /note= "polymorphic amino acid Pro or Leu"
FT Domain 200..222
FT Domain /label= transmembrane_domain
FT Domain 223..417
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FT /label = IC_domain
FT Misc-difference 312
FT /note= "polymorphic amino acid Ala or Arg"
FT Misc-difference 370
FT /note= "polymorphic amino acid Arg or Leu"
FT Misc-difference 381
FT /note= "polymorphic amino acid Arg or His"
XX
PN W02003013581-A1.
XX
XX 20-FEB-2003.
XX
XX 31-JUL-2002; 2002W0-IB003418.
XX
XX 03-AUG-2001; 2001US-0309818P.
XX
XX (GEST ) GENSET SA.
XX
XX Lucas J, Dialynas D, Briggs K;
XX
XX WPI; 2003-268159/26.
XX
XX N-PSDB; ADA00737.
XX
XX New use of Genceptin agonists or antagonists for treating or preventing
XX obesity-related diseases or disorders.
XX
XX Disclosure; Page 33-34; 37pp; English.
XX
CC The present invention describes the use of an agonist or antagonist of
CC GENCEPTIN activity for preventing or treating obesity. Also described is
CC a method of screening for GENCEPTIN activity such as lipid partitioning,
CC lipid metabolism, insulin-like activity, free fatty acid oxidation, and
CC weight reduction. GENCEPTIN has anorectic, antilipemic,
CC antiarteriosclerotic, cardiant, antidiabetic, hypotensive,
CC ophthalmological, neuroprotective and nephrotropic activities. GENCEPTIN
CC can be used for treating or preventing obesity-related diseases or
CC disorders, e.g. obesity, insulin resistance, atherosclerosis,
CC atheromatous disease, heart disease (e.g. cardiac insufficiency, coronary
CC insufficiency, high blood pressure), hypertension, stroke, syndrome X,
CC diabetes mellitus (type I and II), hyperlipidaemia and hyperuricaemia,
CC also diabetic complications, e.g. microangiopathic lesions, ocular
CC lesions, retinopathy, neuropathy and renal lesions. The present sequence
CC represents human GENCEPTIN, which is given in the exemplification of the
CC present invention.
XX
XX Sequence 417 AA;
SQ
Query Match 100.0%; Score 2323; DB 6; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEQPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
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|
|
Db 1 MEQPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
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|
|
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCSSAVADTRCGCKPG 120
|
|
|
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNSECARCOACDEQASQVALENCSSAVADTRCGCKPG 120
|
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|
QY 121 WFVECVQSCVSSPPFYCPCLDCGALHRRHRLCSRRDTCGTCPLPGFYEHGDCVSCP 180
|
|
|
Db 121 WFVECVQSCVSSPPFYCPCLDCGALHRRHRLCSRRDTCGTCPLPGFYEHGDCVSCP 180
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QY 181 TSTLGSCTPCERCAAVCGWRQFWQVLLAGLVLLIGATLTYTTRHCWPHKPLVTADDEAG 240
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|
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Db 181 TSTLGSCTPCERCAAVCGWRQFWQVLLAGLVLLIGATLTYTTRHCWPHKPLVTADDEAG 240
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QY 241 MEALTTPPPATHLSPLDSAHLLAPPDSSSEKICTVQLVGNSSWTPGYPETQALCPQVTWSW 300
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|
|
Db 241 MEALTTPPPATHLSPLDSAHLLAPPDSSSEKICTVQLVGNSSWTPGYPETQALCPQVTWSW 300
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QY 301 DQLPSRALGPAAAPTLSPESSPAGSPAMMLQPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
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|
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Db 301 DQLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLEAE 360
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Db 361 IEAVEVEIGRFRDQOQYEMLKRWKQQPAGLGAVYAALERMGLDGCVEDLSRLQGP 417

RESULT 15
ID ABG73824
XX ABG73824 standard; protein; 417 AA.
AC ABG73824;
XX
DT 27-MAR-2003 (first entry)
XX
DE Human apoptotic protein, Apo-3.
XX
KW human; Apo-2 ligand inhibitor; Apo-2LI; apoptosis; NF-kappaB; JNK;
KW c-Jun N-terminal kinase; necrosis factor kappa B; chimeric molecule;
KW tissue-specific typing; Apo-3; transgenic; affinity purification;
KW competitive-type receptor binding assay.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..198
FT /label= Extracellular_domain
FT Protein 1..181
FT /label= Apo-2LI
FT /note= "Specifically claimed in claim 4. Residues 1-181
FT of Apo-3 represent Apo2LI"
FT 34..71
FT /label= Cysteine-rich_domain_1
FT 72..115
FT /label= Cysteine-rich_domain_2
FT 116..163
FT /label= Cysteine-rich_domain_3
FT 164..181
FT /label= Cysteine-rich_domain_4
FT /note= "This cysteine-rich domain is apparently truncated
FT in Apo-2LI and contains only 3 cysteines instead of 6."
FT 338..417
FT /label= Death_domain

US2002146768-A1.
XX
PD 10-OCT-2002.
XX
PF 19-NOV-2001; 2001US-00993234.
XX
PR 01-APR-1996; 96US-00625328.
PR 23-SEP-1996; 96US-00710802.
PR 31-MAR-1997; 97US-00828683.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ;
XX
DR WPI; 2003-174176/17.
DR N-PSDB; ABX15507, ABX15003.
XX
PT New isolated biologically active Apo-2LI or Apo-3 used to induce
PT apoptosis in mammalian cells.
XX
PS Claim 22; Fig 4; 44pp; English.
XX
CC The invention relates to an isolated biologically active Apo-2LI or Apo-3
CC which has at least 80% sequence identity with native sequence Apo-2LI
CC having 1-181 amino acids or Apo-3 having 1-417 amino acids, respectively.
CC Apo-3 can be employed therapeutically to induce apoptosis or NF-kappaB or
CC JNK mediated gene expression in mammalian cells. The Apo-3 chimeric
CC molecules can be employed therapeutically to inhibit apoptosis; necrosis
CC factor (NF)-kappaB induction; c-Jun N-terminal kinase (JNK) activation.

CC Apo-2LI can be employed therapeutically to inhibit mammalian cell
CC apoptosis in vivo or ex vivo. Nucleic acid sequences encoding the Apo-3
CC or Apo-2LI may be used as a diagnostic for tissue-specific typing. The
CC isolated Apo-3 or Apo-2LI may be used in quantitative diagnostic assays
CC as a control against which samples containing unknown quantities of Apo-3
CC or Apo-2LI may be prepared. Apo-3 preparations are also useful in
CC generating antibodies, as standards in assays for Apo-3 or Apo-2LI, in
CC affinity purification techniques, and in competitive-type receptor
CC binding assays when labelled with, e.g. radioiodine, enzymes, or
CC fluorophores. Modified forms of the Apo-3, e.g. Apo-3-IgG chimeric
CC molecules can be used as immunogens in producing anti-Apo-3 antibodies.
CC Nucleic acids which encode Apo-3 or its modified forms can also be used
CC to generate either transgenic animals or knock out animals, e.g. mouse or
CC rat, which, in turn, are useful in the development and screening of
CC therapeutically useful reagents. The Apo-3 polypeptide stimulates or
CC induces apoptotic activity in mammalian cells. The present sequence
CC represents the human apoptotic protein, Apo-3. Residues 1-181 of Apo3
CC represent Apo2LI which may be a secreted or soluble form of Apo3
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 2323; DB 6; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEQRPRGCAAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQRPRGCAAAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCSAVADTRCGCKPG 120
QY 121 WFVEQCVSQCVSPPYFCPLDCGALHRRHLLCSRRDTCGTLPGFYEHDGCVSCP 180
Db 121 WFVEQCVSQCVSPPYFCPLDCGALHRRHLLCSRRDTCGTLPGFYEHDGCVSCP 180
QY 181 TSTLGSCPERCAAVCGMRQMFVQVLLAGLVPLLLGATLTYTTRHCWPHKPLVTADAG 240
Db 181 TSTLGSCPERCAAVCGMRQMFVQVLLAGLVPLLLGATLTYTTRHCWPHKPLVTADAG 240
QY 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVQLVGNHSWTGYPETQALCPQVTWSW 300
Db 241 MEALTPPPATHLSPLDSAHLLAPPDSSEKICTVQLVGNHSWTGYPETQALCPQVTWSW 300
QY 301 DQLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLEAE 360
Db 301 DQLPSRALGPAAPTLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLEAE 360
QY 361 IEAVEVEIGRFRDQOQYEMLKRWKQQPAGLGAVYAALERMGLDGCVEDLSRLQGP 417
Db 361 IEAVEVEIGRFRDQOQYEMLKRWKQQPAGLGAVYAALERMGLDGCVEDLSRLQGP 417

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GenCore version 5.1.7
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OM protein - protein search, using sw model

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Title: US-10-081-280-6

Perfect score: 2323

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- Published Applications_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2323	100.0	417	3	US-09-314-889-4
5	2323	100.0	417	4	US-10-005-842-5
6	2323	100.0	417	4	US-10-081-280-6
7	2323	100.0	417	4	US-10-112-793-6
8	2323	100.0	417	4	US-10-112-193-10
9	2323	100.0	417	4	US-10-175-902-5
10	2323	100.0	417	4	US-10-189-189-4
11	2323	100.0	417	4	US-10-210-951-24
12	2323	100.0	417	4	US-10-211-884-24
13	2323	100.0	417	4	US-10-310-793-4
14	2323	100.0	417	4	US-10-211-858-24
15	2323	100.0	417	4	US-10-415-247-3
16	2323	100.0	417	4	US-10-648-825-5
17	2323	100.0	417	4	US-10-774-622-5
18	2323	100.0	417	4	US-10-744-379-2
19	2323	100.0	417	5	US-10-979-831-5
20	2323	100.0	833	4	US-10-226-296-5
21	2323	100.0	833	4	US-10-226-318-5
22	2323	100.0	833	4	US-10-648-786-5
23	2323	100.0	833	5	US-10-648-786-5
24	2267	97.6	428	3	US-09-333-966-2
25	2267	97.6	428	3	US-09-314-889-2
26	2267	97.6	428	4	US-10-189-189-2
27	1404	60.4	411	4	US-10-744-379-6

28	1051	45.2	181	3	US-09-884-733-1	Sequence 1, Appli
29	1051	45.2	181	3	US-09-993-234-1	Sequence 1, Appli
30	1051	45.2	181	4	US-10-081-280-1	Sequence 1, Appli
31	1051	45.2	181	4	US-10-112-793-1	Sequence 1, Appli
32	1051	45.2	181	4	US-10-112-193-1	Sequence 1, Appli
33	1051	45.2	188	4	US-10-415-247-5	Sequence 5, Appli
34	404.5	17.4	454	4	US-10-410-012-3	Sequence 3, Appli
35	404.5	17.4	454	4	US-10-799-345-24	Sequence 24, Appli
36	394.5	17.0	461	4	US-10-748-112-21	Sequence 21, Appli
37	387.5	16.7	471	3	US-09-970-532-2	Sequence 2, Appli
38	381	16.4	74	3	US-09-887-879-15	Sequence 15, Appli
39	381	16.4	74	3	US-09-992-964-15	Sequence 15, Appli
40	381	16.4	74	4	US-10-207-295-9	Sequence 9, Appli
41	381	16.4	74	4	US-10-242-383-15	Sequence 15, Appli
42	380.5	16.4	461	3	US-09-899-422-15	Sequence 15, Appli
43	380.5	16.4	461	3	US-09-898-234-15	Sequence 15, Appli
44	380.5	16.4	461	3	US-09-899-429A-25	Sequence 25, Appli
45	380.5	16.4	461	3	US-09-792-356-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1

US-09-333-966-4
; Sequence 4, Application US/09333966
; Patent No. US20020009773A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/333,966
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,469
; FILING DATE:
; APPLICATION NUMBER: No. US20020009773A1 Yet Assigned
; FILING DATE: 06-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-333-966-4

Query Match
Best Local Similarity 100.0%; Score 2323; DB 3; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKI GLFCCRCGPAGHYLKAP 60
Db 1 MEORPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKI GLFCCRCGPAGHYLKAP 60

QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCSSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCSSAVADTRCGCKPG 120

QY 121 WFVECVQSCVSSSPFYCPCLDCGALHRRHRLLCRRDTCGTCLPGFYEHGDCGVSCP 180
Db 121 WFVECVQSCVSSSPFYCPCLDCGALHRRHRLLCRRDTCGTCLPGFYEHGDCGVSCP 180

QY 181 TSTLGSCEPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPKPLVTAD EAG 240
Db 181 TSTLGSCEPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPKPLVTAD EAG 240

QY 241 MEALTPPPATHLSPLDSHTLLAPPDSSEKI CTIVQLVGNSWTPGYPETQALCPQVTWSW 300
Db 241 MEALTPPPATHLSPLDSHTLLAPPDSSEKI CTIVQLVGNSWTPGYPETQALCPQVTWSW 300

QY 301 DQLPSRALGPAAAPTILSPESPAGSPAMMLQPGPOLYDVMNDVAVPARRWKEFVRTLGLREAE 360
Db 301 DQLPSRALGPAAAPTILSPESPAGSPAMMLQPGPOLYDVMNDVAVPARRWKEFVRTLGLREAE 360

QY 361 IEAVEVEIGRFRDQYEMLRKWRQQQPGAGLVAVYALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFRDQYEMLRKWRQQQPGAGLVAVYALERMGLDGCVEDLRSRLQRP 417

RESULT 2
US-09-874-138-5
; Sequence 5, Application US/09874138
; Patent No. US20020072091A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Yu, Guo-liang
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Death Domain Containing Receptor 5
; FILE REFERENCE: 1488.131006
; CURRENT APPLICATION NUMBER: US/09/874,138
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/565,009
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/148,939
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: 60/133,238
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/132,498
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 09/042,583
; PRIOR FILING DATE: 1998-03-17
; PRIOR APPLICATION NUMBER: 60/054,021
; PRIOR FILING DATE: 1997-07-29
; PRIOR APPLICATION NUMBER: 60/040,846
; PRIOR FILING DATE: 1997-03-17
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-874-138-5

Query Match
100.0%; Score 2323; DB 3; Length 417;

; TOPOLOGY: linear
; MOLECULE TYPE: protein
us-10-081-280-6.rapbm

Best Local Similarity 100.0%; Pred. No. 5.7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKI GLFCCRCGPAGHYLKAP 60
Db 1 MEORPRGCAVAALLLVLLGARAQGGTRSPRCDCAGDFHKKI GLFCCRCGPAGHYLKAP 60

QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCSSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHNSCARCOACDEQASQVALENCSSAVADTRCGCKPG 120

QY 121 WFVECVQSCVSSSPFYCPCLDCGALHRRHRLLCRRDTCGTCLPGFYEHGDCGVSCP 180
Db 121 WFVECVQSCVSSSPFYCPCLDCGALHRRHRLLCRRDTCGTCLPGFYEHGDCGVSCP 180

QY 181 TSTLGSCEPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPKPLVTAD EAG 240
Db 181 TSTLGSCEPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPKPLVTAD EAG 240

QY 241 MEALTPPPATHLSPLDSHTLLAPPDSSEKI CTIVQLVGNSWTPGYPETQALCPQVTWSW 300
Db 241 MEALTPPPATHLSPLDSHTLLAPPDSSEKI CTIVQLVGNSWTPGYPETQALCPQVTWSW 300

QY 301 DQLPSRALGPAAAPTILSPESPAGSPAMMLQPGPOLYDVMNDVAVPARRWKEFVRTLGLREAE 360
Db 301 DQLPSRALGPAAAPTILSPESPAGSPAMMLQPGPOLYDVMNDVAVPARRWKEFVRTLGLREAE 360

QY 361 IEAVEVEIGRFRDQYEMLRKWRQQQPGAGLVAVYALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFRDQYEMLRKWRQQQPGAGLVAVYALERMGLDGCVEDLRSRLQRP 417

RESULT 3
US-09-993-234-6
; Sequence 6, Application US/09993234
; Patent No. US20020146768A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/993,234
; FILING DATE: 19-No. US20020146768A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,683
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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US-09-993-234-6

Query Match 100.0%; Score 2323; DB 3; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORPRGCAAAVALLVLLGARAAGGTRSPRCDACAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEORPRGCAAAVALLVLLGARAAGGTRSPRCDACAGDFHKKIGLFCRCGCPAGHYLKAP 60

QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCCCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCCCKPG 120

QY 121 WFVEQVQSCVSSSPFYCOPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHDGCVSCP 180
DB 121 WFVEQVQSCVSSSPFYCOPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHDGCVSCP 180

QY 181 TSTLGSCEPERCAAAVALLVLLGARAAGGTRSPRCDACAGDFHKKIGLFCRCGCPAGHYLKAP 240
DB 181 TSTLGSCEPERCAAAVALLVLLGARAAGGTRSPRCDACAGDFHKKIGLFCRCGCPAGHYLKAP 240

QY 241 MEALTPPPATHLSPLDSAHLLAPPDSEKICTVQLVGNSTPGYPTQALCPQVTSW 300
DB 241 MEALTPPPATHLSPLDSAHLLAPPDSEKICTVQLVGNSTPGYPTQALCPQVTSW 300

QY 301 DQPSRALGPAAAPTLSPEPAGSPAMMLOPQPOLVDVMDVAPARWKEFVRTLGLREAE 360
DB 301 DQPSRALGPAAAPTLSPEPAGSPAMMLOPQPOLVDVMDVAPARWKEFVRTLGLREAE 360

QY 361 IEAVEVEIGRFRDQYEMLRWRQOQAGLVAVYALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFRDQYEMLRWRQOQAGLVAVYALERMGLDGCVEDLRSRLQRP 417

RESULT 4

US-09-314-889-4
; Sequence 4, Application US/09314889
; Publication No. US20030077694A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/314,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/815,469
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,711
; FILING DATE: 17-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,285
; FILING DATE: 12-MAR-1996
; ATTORNEY/AGENT INFORMATION:

NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-314-889-4

Query Match 100.0%; Score 2323; DB 3; Length 417;

Best Local Similarity 100.0%; Pred. No. 5.7e-163;

Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORPRGCAAAVALLVLLGARAAGGTRSPRCDACAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEORPRGCAAAVALLVLLGARAAGGTRSPRCDACAGDFHKKIGLFCRCGCPAGHYLKAP 60

QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCCCKPG 120
DB 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCCCKPG 120

QY 121 WFVEQVQSCVSSSPFYCOPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHDGCVSCP 180
DB 121 WFVEQVQSCVSSSPFYCOPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHDGCVSCP 180

QY 181 TSTLGSCEPERCAAAVALLVLLGARAAGGTRSPRCDACAGDFHKKIGLFCRCGCPAGHYLKAP 240
DB 181 TSTLGSCEPERCAAAVALLVLLGARAAGGTRSPRCDACAGDFHKKIGLFCRCGCPAGHYLKAP 240

QY 241 MEALTPPPATHLSPLDSAHLLAPPDSEKICTVQLVGNSTPGYPTQALCPQVTSW 300
DB 241 MEALTPPPATHLSPLDSAHLLAPPDSEKICTVQLVGNSTPGYPTQALCPQVTSW 300

QY 301 DQPSRALGPAAAPTLSPEPAGSPAMMLOPQPOLVDVMDVAPARWKEFVRTLGLREAE 360
DB 301 DQPSRALGPAAAPTLSPEPAGSPAMMLOPQPOLVDVMDVAPARWKEFVRTLGLREAE 360

QY 361 IEAVEVEIGRFRDQYEMLRWRQOQAGLVAVYALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFRDQYEMLRWRQOQAGLVAVYALERMGLDGCVEDLRSRLQRP 417

RESULT 5

US-10-005-842-5
; Sequence 5, Application US/10005842
; Publication No. US20020098550A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; Gentz, Reiner
; Yu, Guo-Liang
; Su, Jeffrey
; Rosen, Craig A.
; TITLE OF INVENTION: Death Domain Containing Receptor 5
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/005,842

; FILING DATE: 07-Dec-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/042,583
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: US 60/040,846
 ; FILING DATE: 17-MAR-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hoover, Kenley
 ; REGISTRATION NUMBER: 40,302
 ; REFERENCE/DOCKET NUMBER: PF366
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 3013098504
 ; TELEFAX: 3013098439
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 417 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-10-005-842-5

Query Match 100.0%; Score 2323; DB 4; Length 417;
 Best Local Similarity 100.0%; Pred. No. 5.7e-163;
 Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEQRPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKI GLGCCRCGPAGHYLKAP 60
 Db 1 MEQRPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKI GLGCCRCGPAGHYLKAP 60
 QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG 120
 Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG 120
 QY 121 WFVECVQSCVSSSPFYCQCLDCGALHRRHTRLLCSRRTDCGTC LFGFVEHGDGCVSCP 180
 Db 121 WFVECVQSCVSSSPFYCQCLDCGALHRRHTRLLCSRRTDCGTC LFGFVEHGDGCVSCP 180
 QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLGATLTYTYRHCHWPHKPLVTAD EAG 240
 Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLGATLTYTYRHCHWPHKPLVTAD EAG 240
 QY 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQ EALCPQVTWSW 300
 Db 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQ EALCPQVTWSW 300
 QY 301 DQLPSRAGPAAAPTLSPEPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAE 360
 Db 301 DQLPSRAGPAAAPTLSPEPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAE 360
 QY 361 IEAVEVEIGRFRDQOYEMLKRWRQQQAGLVAVYALERMGLDGCVEDLRSRLQRP 417
 Db 361 IEAVEVEIGRFRDQOYEMLKRWRQQQAGLVAVYALERMGLDGCVEDLRSRLQRP 417

RESULT 6
 US-10-081-280-6
 ; Sequence 6, Application US/10081280
 ; Publication No. US20020165157A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/081,280
 ; FILING DATE: 21-Feb-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/829,270
 ; FILING DATE: 31-Mar-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Matschang, Diane L.
 ; REGISTRATION NUMBER: 35,600
 ; REFERENCE/DOCKET NUMBER: F1007R1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-5416
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 417 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-10-081-280-6

Query Match 100.0%; Score 2323; DB 4; Length 417;
 Best Local Similarity 100.0%; Pred. No. 5.7e-163;
 Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEQRPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKI GLGCCRCGPAGHYLKAP 60
 Db 1 MEQRPRGCAVAAALLVLLGARAQGGTRSPRCDCAGDFHKKI GLGCCRCGPAGHYLKAP 60
 QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG 120
 Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG 120
 QY 121 WFVECVQSCVSSSPFYCQCLDCGALHRRHTRLLCSRRTDCGTC LFGFVEHGDGCVSCP 180
 Db 121 WFVECVQSCVSSSPFYCQCLDCGALHRRHTRLLCSRRTDCGTC LFGFVEHGDGCVSCP 180
 QY 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLGATLTYTYRHCHWPHKPLVTAD EAG 240
 Db 181 TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLGATLTYTYRHCHWPHKPLVTAD EAG 240
 QY 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQ EALCPQVTWSW 300
 Db 241 MEALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQ EALCPQVTWSW 300
 QY 301 DQLPSRAGPAAAPTLSPEPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAE 360
 Db 301 DQLPSRAGPAAAPTLSPEPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAE 360
 QY 361 IEAVEVEIGRFRDQOYEMLKRWRQQQAGLVAVYALERMGLDGCVEDLRSRLQRP 417
 Db 361 IEAVEVEIGRFRDQOYEMLKRWRQQQAGLVAVYALERMGLDGCVEDLRSRLQRP 417

RESULT 7
 US-10-112-793-6
 ; Sequence 6, Application US/10112793
 ; Publication No. US20020192729A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,793
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,683A
FILING DATE: 31-Mar-1997
APPLICATION NUMBER: 08/625328
FILING DATE: 1-Apr-1996
APPLICATION NUMBER: 08/710802
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1007P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-112-793-6

Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEQPRGCAAAVAAALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQPRGCAAAVAAALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCNSAVADTRCGCKPG 120
DB 61 CTEPCGNSCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVECVQSCVSSSPFYCPQCLDCGALHRRHLLCSRRDTCGTCLPGFYEHDGCVSCP 180
DB 121 WFVECVQSCVSSSPFYCPQCLDCGALHRRHLLCSRRDTCGTCLPGFYEHDGCVSCP 180
QY 181 TSTLGSCEPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTRHCWPHKPLVTAD 240
DB 181 TSTLGSCEPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTRHCWPHKPLVTAD 240
QY 241 MEALTPPPATHLSPLDSAHLLAPPDSSSEKICTVQLVGNWSTPGYPTQALCPQVTWSW 300
DB 241 MEALTPPPATHLSPLDSAHLLAPPDSSSEKICTVQLVGNWSTPGYPTQALCPQVTWSW 300
QY 301 DQLPSPALGPAAPATLSPSPAGSPAMMLQPGPQLYDVMNDVAPARWKEFVRTLGLREAE 360
DB 301 DQLPSPALGPAAPATLSPSPAGSPAMMLQPGPQLYDVMNDVAPARWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQYEMLRKRWQQAQAGLVAVYALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFRDQYEMLRKRWQQAQAGLVAVYALERMGLDGCVEDLRSRLQRP 417

RESULT 8
US-10-112-193-10
; Sequence 10, Application US/10112193
; Publication No. US20030004313A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE

NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,193
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,069
FILING DATE: 11-Sep-1997
APPLICATION NUMBER: 60/026943
FILING DATE: 23-Sep-1996
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1052R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-112-193-10

Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEQPRGCAAAVAAALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
DB 1 MEQPRGCAAAVAAALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCNSAVADTRCGCKPG 120
DB 61 CTEPCGNSCLVCPQDTFLAWENHNHSECARQACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVECVQSCVSSSPFYCPQCLDCGALHRRHLLCSRRDTCGTCLPGFYEHDGCVSCP 180
DB 121 WFVECVQSCVSSSPFYCPQCLDCGALHRRHLLCSRRDTCGTCLPGFYEHDGCVSCP 180
QY 181 TSTLGSCEPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTRHCWPHKPLVTAD 240
DB 181 TSTLGSCEPERCAAVCGWRQMFVQVLLAGLVVPLLIGATLTYTRHCWPHKPLVTAD 240
QY 241 MEALTPPPATHLSPLDSAHLLAPPDSSSEKICTVQLVGNWSTPGYPTQALCPQVTWSW 300
DB 241 MEALTPPPATHLSPLDSAHLLAPPDSSSEKICTVQLVGNWSTPGYPTQALCPQVTWSW 300
QY 301 DQLPSPALGPAAPATLSPSPAGSPAMMLQPGPQLYDVMNDVAPARWKEFVRTLGLREAE 360
DB 301 DQLPSPALGPAAPATLSPSPAGSPAMMLQPGPQLYDVMNDVAPARWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQYEMLRKRWQQAQAGLVAVYALERMGLDGCVEDLRSRLQRP 417
DB 361 IEAVEVEIGRFRDQYEMLRKRWQQAQAGLVAVYALERMGLDGCVEDLRSRLQRP 417

RESULT 9
US-10-175-902-5
; Sequence 5, Application US/10175902

Publication No. US20030108516A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rozen, Craig A.
; APPLICANT: Pan, James G.
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dixit, Vishva M.
; TITLE OF INVENTION: Death Domain Containing Receptor 4
; FILE REFERENCE: 1488.130005
; CURRENT APPLICATION NUMBER: US/10/175,902
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 09/565,918
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: US 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: US 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: US 60/035,722
; PRIOR FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-175-902-5

Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEORPRGCAVAAALLVLLGARAQGGTSPRCDCAGDFHKKI GLGCCRCGPAGHYLKAP	60
DB	1	MEORPRGCAVAAALLVLLGARAQGGTSPRCDCAGDFHKKI GLGCCRCGPAGHYLKAP	60
QY	61	CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG	120
DB	61	CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG	120
QY	121	WFVEQCVSQVSSSPFYCQCLDCGALHRRHRLCSRRDTCCTCLPGFYEHDGCVSCP	180
DB	121	WFVEQCVSQVSSSPFYCQCLDCGALHRRHRLCSRRDTCCTCLPGFYEHDGCVSCP	180
QY	181	TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLITYYRHCHWPHKPLVTAD	240
DB	181	TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLITYYRHCHWPHKPLVTAD	240
QY	241	MEALTTPPPATHLSPLDSAHTLLAPPDSSEKI CTIVQLVGNSWTGYPETQALCPQVTWSW	300
DB	241	MEALTTPPPATHLSPLDSAHTLLAPPDSSEKI CTIVQLVGNSWTGYPETQALCPQVTWSW	300
QY	301	DQLPSRALGPAAPTLLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLEAE	360
DB	301	DQLPSRALGPAAPTLLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLEAE	360
QY	361	IEAVEVEIGRFRDQOQYEMLKRWRQOQAPAGIAGVYAALERMGLDGCVEDLRSRLQRP	417
DB	361	IEAVEVEIGRFRDQOQYEMLKRWRQOQAPAGIAGVYAALERMGLDGCVEDLRSRLQRP	417

RESULT 10
US-10-189-189-4
; Sequence 4, Application US/10189189
; Publication No. US20030170203A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Dixit, Vishva
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Dillon, Patrick J.
; TITLE OF INVENTION: Death Domain Containing Receptors

FILE REFERENCE: 1488.031000C
; CURRENT APPLICATION NUMBER: US/10/189,189
; CURRENT FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: US 60/314,314
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/303,155
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 09/557,908
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: US 60/136,741
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 60/130,488
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: US 08/815,469
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: US 60/037,341
; PRIOR FILING DATE: 1997-02-06
; PRIOR APPLICATION NUMBER: US 60/028,711
; PRIOR FILING DATE: 1996-10-17
; PRIOR APPLICATION NUMBER: US 60/013,285
; PRIOR FILING DATE: 1996-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-189-189-4

Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEORPRGCAVAAALLVLLGARAQGGTSPRCDCAGDFHKKI GLGCCRCGPAGHYLKAP	60
DB	1	MEORPRGCAVAAALLVLLGARAQGGTSPRCDCAGDFHKKI GLGCCRCGPAGHYLKAP	60
QY	61	CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG	120
DB	61	CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG	120
QY	121	WFVEQCVSQVSSSPFYCQCLDCGALHRRHRLCSRRDTCCTCLPGFYEHDGCVSCP	180
DB	121	WFVEQCVSQVSSSPFYCQCLDCGALHRRHRLCSRRDTCCTCLPGFYEHDGCVSCP	180
QY	181	TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLITYYRHCHWPHKPLVTAD	240
DB	181	TSTLGSCPERCAAVCGWRQMFVQVLLAGLVPLLLGATLITYYRHCHWPHKPLVTAD	240
QY	241	MEALTTPPPATHLSPLDSAHTLLAPPDSSEKI CTIVQLVGNSWTGYPETQALCPQVTWSW	300
DB	241	MEALTTPPPATHLSPLDSAHTLLAPPDSSEKI CTIVQLVGNSWTGYPETQALCPQVTWSW	300
QY	301	DQLPSRALGPAAPTLLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLEAE	360
DB	301	DQLPSRALGPAAPTLLSPSPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLEAE	360
QY	361	IEAVEVEIGRFRDQOQYEMLKRWRQOQAPAGIAGVYAALERMGLDGCVEDLRSRLQRP	417
DB	361	IEAVEVEIGRFRDQOQYEMLKRWRQOQAPAGIAGVYAALERMGLDGCVEDLRSRLQRP	417

RESULT 11
US-10-210-951-24
; Sequence 24, Application US/10210951
; Publication No. US20030170228A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.

APPLICANT: Pan, James
APPLICANT: Pitti, Robert M.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stone, Donna M.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
FILE REFERENCE: P2931R1C1
CURRENT APPLICATION NUMBER: US/10/210,951
CURRENT FILING DATE: 2002-08-02
PRIOR FILING DATE: 1996-04-01
PRIOR APPLICATION NUMBER: 60/014699
PRIOR FILING DATE: 1996-04-01
PRIOR APPLICATION NUMBER: 60/026943
PRIOR FILING DATE: 1996-09-23
PRIOR APPLICATION NUMBER: 60/059121
PRIOR FILING DATE: 1997-07-17
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/062037
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066772
PRIOR FILING DATE: 1997-11-24
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 258
SEQ ID NO 24
LENGTH: 417
TYPE: PRT
ORGANISM: Homo sapiens
US-10-210-951-24

Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEORPRGCAAAVALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEORPRGCAAAVALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTBPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTBPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCASAVADTRCGCKPG 120

Qy 121 WFVECVQSCVSSPPFYCQCLDCGALHRRHRLCSRRDTCGTCCLPGFYEHDGCVSCP 180
Db 121 WFVECVQSCVSSPPFYCQCLDCGALHRRHRLCSRRDTCGTCCLPGFYEHDGCVSCP 180

Qy 181 TSTLGSCTPCERCAAVCGWRQFWQVLLAGLVVPLLIGATLITYYRHCPHKLPLVTAD 240
Db 181 TSTLGSCTPCERCAAVCGWRQFWQVLLAGLVVPLLIGATLITYYRHCPHKLPLVTAD 240

Qy 241 MEALTPPPATHLSPLDSANTLLAPPDSSEKICTVQLVGNSTPGYPTQALCPQVTWSW 300
Db 241 MEALTPPPATHLSPLDSANTLLAPPDSSEKICTVQLVGNSTPGYPTQALCPQVTWSW 300

Qy 301 DOLPSRALGPAAPTLSPSPAGSPAMMLOPGPOLYDMDAVPARRKKEFVRLTGLREAE 360
Db 301 DOLPSRALGPAAPTLSPSPAGSPAMMLOPGPOLYDMDAVPARRKKEFVRLTGLREAE 360

Qy 361 IEAVEVEIGFRDQOQYEMLXKRWQOQAGLGA VVAALERMGLDGCVEDLSRLQRP 417
Db 361 IEAVEVEIGFRDQOQYEMLXKRWQOQAGLGA VVAALERMGLDGCVEDLSRLQRP 417

US-10-211-884-24
Sequence 24, Application US/10211884
Publication No. US20030175900A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Pitti, Robert M.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stone, Donna M.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
FILE REFERENCE: P2931R1C1
CURRENT APPLICATION NUMBER: US/10/211,884
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: 60/014699
PRIOR FILING DATE: 1996-04-01
PRIOR APPLICATION NUMBER: 60/026943
PRIOR FILING DATE: 1996-09-23
PRIOR APPLICATION NUMBER: 60/059121
PRIOR FILING DATE: 1997-07-17
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/062037
PRIOR FILING DATE: 1997-10-10
PRIOR APPLICATION NUMBER: 60/063755
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063045
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/066511
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066772
PRIOR FILING DATE: 1997-11-24
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 258
SEQ ID NO 24
LENGTH: 417
TYPE: PRT
ORGANISM: Homo sapiens
US-10-211-884-24

Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEORPRGCAAAVALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEORPRGCAAAVALLVLLGARAQGGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60

Qy 61 CTBPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTBPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCASAVADTRCGCKPG 120

Qy 121 WFVECVQSCVSSPPFYCQCLDCGALHRRHRLCSRRDTCGTCCLPGFYEHDGCVSCP 180
Db 121 WFVECVQSCVSSPPFYCQCLDCGALHRRHRLCSRRDTCGTCCLPGFYEHDGCVSCP 180

Qy 181 TSTLGSCTPCERCAAVCGWRQFWQVLLAGLVVPLLIGATLITYYRHCPHKLPLVTAD 240
Db 181 TSTLGSCTPCERCAAVCGWRQFWQVLLAGLVVPLLIGATLITYYRHCPHKLPLVTAD 240

Qy 241 MEALTPPPATHLSPLDSANTLLAPPDSSEKICTVQLVGNSTPGYPTQALCPQVTWSW 300
Db 241 MEALTPPPATHLSPLDSANTLLAPPDSSEKICTVQLVGNSTPGYPTQALCPQVTWSW 300

QY 301 DQPSRAGPAAAPTLLSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
Db 301 DQPSRAGPAAAPTLLSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEIGRFRDQOQYEMLRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQGP 417
Db 361 IEAVEIGRFRDQOQYEMLRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQGP 417

RESULT 13
US-10-310-793-4
; Sequence 4, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
; FILE REFERENCE: P5573
; CURRENT APPLICATION NUMBER: US/10/310,793
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 417
; TYPE: PRT
; ORGANISM: human
US-10-310-793-4

Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORPRGCAVAALLLVLLGARAQGGTRSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEORPRGCAVAALLLVLLGARAQGGTRSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECAQCACDEQASQVALENCNSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNSECAQCACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVEQVQSVSSPFFCQCLDCGALHRTLLCSRRDTCGTCLPGFVHEHGDGCVSCP 180
Db 121 WFVEQVQSVSSPFFCQCLDCGALHRTLLCSRRDTCGTCLPGFVHEHGDGCVSCP 180
QY 181 TSTLGSCEPCAAVCGWRQFWQVLLAGLVVPLLIGATLTYTYRHCWPKHPLVTADEAG 240
Db 181 TSTLGSCEPCAAVCGWRQFWQVLLAGLVVPLLIGATLTYTYRHCWPKHPLVTADEAG 240

QY 241 MEATPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWPGYPETQALCPQVTWSW 300
Db 241 MEATPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSTWPGYPETQALCPQVTWSW 300
QY 301 DQPSRAGPAAAPTLLSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
Db 301 DQPSRAGPAAAPTLLSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEIGRFRDQOQYEMLRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQGP 417
Db 361 IEAVEIGRFRDQOQYEMLRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQGP 417

RESULT 14
US-10-211-858-24
; Sequence 24, Application US/10211858
; Publication No. US20030211096A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Pitti, Robert M.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stone, Donna M.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
; FILE REFERENCE: P2931R1C1
; CURRENT APPLICATION NUMBER: US/10/211,858
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/014699
; PRIOR FILING DATE: 1996-04-01
; PRIOR APPLICATION NUMBER: 60/026943
; PRIOR FILING DATE: 1996-09-23
; PRIOR APPLICATION NUMBER: 60/059121
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/062037
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/066511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 258
; SEQ ID NO 24
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-211-858-24

Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEORPRGCAVAALLLVLLGARAQGGTRSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEORPRGCAVAALLLVLLGARAQGGTRSPRCDGAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNSECAQCACDEQASQVALENCNSAVADTRCGCKPG 120

Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVECCVSCVSSPPYCPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHGDCVSCP 180
Db 121 WFVECCVSCVSSPPYCPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHGDCVSCP 180
QY 181 TSTLGSCEPCAAVCGWRQMFVQVLLAGLVVPLLGGATLTYYRHCHWPHKPLVTADAEAG 240
Db 181 TSTLGSCEPCAAVCGWRQMFVQVLLAGLVVPLLGGATLTYYRHCHWPHKPLVTADAEAG 240
QY 241 MEALTPPPATHLSPLDSANTLLAPDSSEKICTVQLVGNWSTPGYPETQALCPQVTSW 300
Db 241 MEALTPPPATHLSPLDSANTLLAPDSSEKICTVQLVGNWSTPGYPETQALCPQVTSW 300
QY 301 DOLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAE 360
Db 301 DOLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQRP 417

RESULT 15
US-10-415-247-3
; Sequence 3, Application US/10415247
; Publication No. US20040013655A1
; GENERAL INFORMATION:
; APPLICANT: Shiozawa, Shunichi
; TITLE OF INVENTION: Genome responsible for chronic rheumatoid arthritis,
; TITLE OF INVENTION: diagnostic method, pathogenicity judging method and
; TITLE OF INVENTION: detection-use diagnostic kit of chronic rheumatoid
; TITLE OF INVENTION: arthritis, and therapeutic method and medicine of
; TITLE OF INVENTION: chronic rheumatoid arthritis
; FILE REFERENCE: TLOPI-2
; CURRENT APPLICATION NUMBER: US/10/415,247
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: JP 2000-324296
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: JP 2001-90546
; PRIOR FILING DATE: 2001-3-27
; PRIOR APPLICATION NUMBER: JP 2001-99990
; PRIOR FILING DATE: 2001-3-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-247-3

Query Match 100.0%; Score 2323; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.7e-163;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEORPRGCAVAAALLVLLGARAQGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEORPRGCAVAAALLVLLGARAQGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAP 60
QY 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCNSAVADTRCGCKPG 120
QY 121 WFVECCVSCVSSPPYCPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHGDCVSCP 180
Db 121 WFVECCVSCVSSPPYCPCLDCGALHRRHLLCSRRDTCGTCLPGFYEHGDCVSCP 180
QY 181 TSTLGSCEPCAAVCGWRQMFVQVLLAGLVVPLLGGATLTYYRHCHWPHKPLVTADAEAG 240
Db 181 TSTLGSCEPCAAVCGWRQMFVQVLLAGLVVPLLGGATLTYYRHCHWPHKPLVTADAEAG 240
QY 241 MEALTPPPATHLSPLDSANTLLAPDSSEKICTVQLVGNWSTPGYPETQALCPQVTSW 300

Db 241 MEALTPPPATHLSPLDSANTLLAPDSSEKICTVQLVGNWSTPGYPETQALCPQVTSW 300
QY 301 DOLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAE 360
Db 301 DOLPSRALGPAAAPTLSPEPAGSPAMMLQPGPOLYDVMDAVPARRWKEFVRTLGLREAE 360
QY 361 IEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAALERMGLDGCVEDLRSRLQRP 417

Search completed: March 20, 2006, 08:02:18
Job time : 74 secs

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GenCore version 5.1.7.
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OM protein - protein search, using sw model

Run on: March 20, 2006, 08:00:54 ; Search time 29 Seconds
(without alignments)
411.577 Million cell updates/sec

Title: US-10-081-280-6

Perfect score: 2323

Sequence: 1 MEQPRPGCAVAAALLVLL.....ERMGLDGCVEDLRSLRQRP 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA_New.*
- 1: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pap.*
 - 2: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pap.*
 - 3: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pap.*
 - 4: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pap.*
 - 5: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pap.*
 - 6: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pap.*
 - 7: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.pap.*
 - 8: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2323	100.0	417	7	US-11-174-467-10
2	2323	100.0	418	6	US-10-512-325-3
3	2323	100.0	418	7	US-11-196-919-2
4	2323	100.0	833	7	US-11-076-187-5
5	1051	45.2	181	7	US-11-174-467-1
6	381	16.4	74	7	US-11-116-746-15
7	374.5	16.1	909	7	US-11-076-187-4
8	374	16.1	455	7	US-11-182-946-3
9	364.5	15.7	453	7	US-11-185-878-5
10	206.5	8.9	283	6	US-10-987-663-4
11	200.5	8.6	161	7	US-11-126-126-2
12	200.5	8.6	161	7	US-11-057-923-3
13	199.5	8.6	335	7	US-11-182-946-7
14	199.5	8.6	669	7	US-11-076-187-3
15	197	8.5	331	7	US-11-185-878-3
16	192	8.3	32	7	US-11-196-919-4
17	191	8.2	411	7	US-11-116-746-11
18	191	8.2	411	7	US-11-245-053-1
19	190	8.2	32	6	US-10-512-325-5
20	172	7.4	1198	6	US-10-453-372-880
21	171.5	7.4	934	6	US-10-453-372-1158
22	166	7.1	435	7	US-11-077-386-19
23	166	7.1	450	7	US-11-077-386-20
24	166	7.1	3597	7	US-11-019-711-6
25	166	7.1	3600	7	US-11-019-711-2

26	164	7.1	399	7	US-11-077-386-18	Sequence 18, Appl
27	163.5	7.0	355	7	US-11-182-946-14	Sequence 14, Appl
28	163.5	7.0	415	7	US-11-182-946-6	Sequence 6, Appl
29	162.5	7.0	334	6	US-10-514-057-6	Sequence 6, Appl
30	162.5	7.0	349	7	US-11-182-946-13	Sequence 13, Appl
31	162.5	7.0	467	7	US-11-185-878-6	Sequence 6, Appl
32	162	7.0	612	6	US-10-453-372-1156	Sequence 1156, Ap
33	161	6.9	418	7	US-11-116-746-14	Sequence 14, Appl
34	161	6.9	468	7	US-11-076-187-2	Sequence 2, Appl
35	160	6.9	468	7	US-10-995-561-907	Sequence 907, App
36	159.5	6.9	350	7	US-11-132-285-41	Sequence 41, Appl
37	159	6.8	229	6	US-10-924-074-8	Sequence 8, Appl
38	159	6.8	237	6	US-10-924-074-6	Sequence 6, Appl
39	158	6.8	1574	6	US-10-055-877-211	Sequence 211, App
40	157	6.8	3690	6	US-10-995-561-1016	Sequence 1016, Ap
41	155.5	6.7	427	7	US-11-182-946-5	Sequence 5, Appl
42	155.5	6.7	427	7	US-11-185-878-4	Sequence 4, Appl
43	155	6.7	78	7	US-11-116-746-16	Sequence 16, Appl
44	155	6.7	3717	6	US-10-821-234-1076	Sequence 1076, Ap
45	152	6.5	3714	6	US-10-995-561-1015	Sequence 1015, Ap

ALIGNMENTS

RESULT 1
US-11-174-467-10
; Sequence 10, Application US/11/174467
; Publication No. US20060041106A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/174,467
; FILING DATE: 06-Jul-2005
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,069
; FILING DATE: 11-Sep-1997
; APPLICATION NUMBER: 60/026943
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1052R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-11-174-467-10

Query Match 100.0%; Score 2323; DB 7; Length 417;
Best Local Similarity 100.0%; Pred. No. 2.1e-175;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MEQPRGCAVAAALLLVLLGARAQGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAVAAALLLVLLGARAQGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDFTFLAWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDFTFLAWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
Qy 121 WFVECVQSVSSSPFFCQPCDCLGALHRRHTRLLCSRDDTDCGTCCLPGFVEHGDGCVSCP 180
Db 121 WFVECVQSVSSSPFFCQPCDCLGALHRRHTRLLCSRDDTDCGTCCLPGFVEHGDGCVSCP 180
Qy 181 TSTLGSCTPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPKHPLVTADDEAG 240
Db 181 TSTLGSCTPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPKHPLVTADDEAG 240
Qy 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQBALCPQVTWSW 300
Db 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQBALCPQVTWSW 300
Qy 301 DQLPSRALGPAAPATLSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Db 301 DQLPSRALGPAAPATLSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Qy 361 IEAVEVEIGFRDQOQYEMLRWQOQPGAGLVAAALERMGLDGCVEDLRSRLQGP 417
Db 361 IEAVEVEIGFRDQOQYEMLRWQOQPGAGLVAAALERMGLDGCVEDLRSRLQGP 417
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RESULT 2

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US-10-512-325-3
; Sequence 3, Application US/10512325
; Publication No. US20060013822A1
; GENERAL INFORMATION:
; APPLICANT: Tittle, Thomas V.
; APPLICANT: Wegmann, Keith W.
; TITLE OF INVENTION: UTILIZATION OF MHC CLASS II BINDING
; TITLE OF INVENTION: MOTIFS IN IMMUNIZATION TO PRODUCE IMMUNE SERUM, MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES AND VACCINES
; FILE REFERENCE: TW 2003.00
; CURRENT APPLICATION NUMBER: US/10/512,325
; CURRENT FILING DATE: 2004-10-22
; PRIOR FILING DATE: 2002-03-22
; PRIOR FILING DATE: 2002-03-22
; PRIOR FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (14)...(32)
; OTHER INFORMATION: Extended peptide shown to be the B cell epitope
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(13)
; OTHER INFORMATION: Peptide fragment
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(32)
; OTHER INFORMATION: Peptide fragment
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (14)...(32)
; OTHER INFORMATION: Peptide fragment
US-10-512-325-3
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Query Match 100.0%; Score 2323; DB 6; Length 418;
Best Local Similarity 100.0%; Pred. No. 2.1e-175;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MEQPRGCAVAAALLLVLLGARAQGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDFTFLAWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDFTFLAWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
Qy 121 WFVECVQSVSSSPFFCQPCDCLGALHRRHTRLLCSRDDTDCGTCCLPGFVEHGDGCVSCP 180
Db 121 WFVECVQSVSSSPFFCQPCDCLGALHRRHTRLLCSRDDTDCGTCCLPGFVEHGDGCVSCP 180
Qy 181 TSTLGSCTPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPKHPLVTADDEAG 240
Db 181 TSTLGSCTPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPKHPLVTADDEAG 240
Qy 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQBALCPQVTWSW 300
Db 241 MEALTPPPATHLSPDLSAHTLLAPPDSSEKICTVQLVGNSTWTPGYPETQBALCPQVTWSW 300
Qy 301 DQLPSRALGPAAPATLSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Db 301 DQLPSRALGPAAPATLSPSPAGSPAMMLOPGPOLYDMDAVPARRWKEFVRTILGLREAE 360
Qy 361 IEAVEVEIGFRDQOQYEMLRWQOQPGAGLVAAALERMGLDGCVEDLRSRLQGP 417
Db 361 IEAVEVEIGFRDQOQYEMLRWQOQPGAGLVAAALERMGLDGCVEDLRSRLQGP 417
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RESULT 3

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US-11-196-919-2
; Sequence 2, Application US/11196919
; Publication No. US2005028223A1
; GENERAL INFORMATION:
; APPLICANT: Tittle, Thomas V.
; APPLICANT: Wegmann, Keith W.
; TITLE OF INVENTION: TR3-SPECIFIC BINDING AGENT AND METHODS
; TITLE OF INVENTION: FOR THEIR USE
; FILE REFERENCE: TW2001.01
; CURRENT APPLICATION NUMBER: US/11/196,919
; CURRENT FILING DATE: 2005-08-04
; PRIOR APPLICATION NUMBER: PCT/US00/31692
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/166,583
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 10/204,419
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-196-919-2
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Query Match 100.0%; Score 2323; DB 7; Length 418;
Best Local Similarity 100.0%; Pred. No. 2.1e-175;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MEQPRGCAVAAALLLVLLGARAQGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAVAAALLLVLLGARAQGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAP 60
Qy 61 CTEPCGNSTCLVCPQDFTFLAWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
Db 61 CTEPCGNSTCLVCPQDFTFLAWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPG 120
Qy 121 WFVECVQSVSSSPFFCQPCDCLGALHRRHTRLLCSRDDTDCGTCCLPGFVEHGDGCVSCP 180
Db 121 WFVECVQSVSSSPFFCQPCDCLGALHRRHTRLLCSRDDTDCGTCCLPGFVEHGDGCVSCP 180
Qy 181 TSTLGSCTPERCAAVCGWRQMFVQVLLAGLVVPLLGLATLTYTYRHCHWPKHPLVTADDEAG 240
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Db 181 TSTLSCPERCAAVCGWRQMFVQVLLAGLVVPLLGATLTYYRHCWPHKPLVTADEAG 240
Qy 241 MEALTTPPPATHSLPDSANTLLAPPDSSEKICTVQVLGNSWTFPGYPTQALCPQVTWSW 300
Db 241 MEALTTPPPATHSLPDSANTLLAPPDSSEKICTVQVLGNSWTFPGYPTQALCPQVTWSW 300
Qy 301 DQLPSPALGPAAPATLSPSPAGSPAMMLQPGQPLQDYVMDVAVPARRWKEFVRTLGLREAE 360
Db 301 DQLPSPALGPAAPATLSPSPAGSPAMMLQPGQPLQDYVMDVAVPARRWKEFVRTLGLREAE 360
Qy 361 IEAVEVEIGRFRDQOQYEMLKRWRQOQAGLGAVYAALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFRDQOQYEMLKRWRQOQAGLGAVYAALERMGLDGCVEDLRSRLQRP 417

RESULT 4

US-11-076-187-5
; Sequence 5, Application US/11076187
; Publication No. US20050244857A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Pan, James G
; APPLICANT: Gentz, Reiner L
; APPLICANT: Dixit, Vishva M
; TITLE OF INVENTION: Death Domain Containing Receptor-4
; FILE REFERENCE: P335P3
; CURRENT APPLICATION NUMBER: US/11/076,187
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: 60/035,722
; PRIOR FILING DATE: 1997-01-28
; PRIOR APPLICATION NUMBER: 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 09/565,918
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/406,922
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/413,861
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 10/648,786
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 60/551,768
; PRIOR FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: 60/608,469
; PRIOR FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-076-187-5

Query Match 100.0%; Score 2323; DB 7; Length 833;
Best Local Similarity 100.0%; Pred. No. 4.5e-175;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQPRGCAVAALVLLGARAQGGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAVAALVLLGARAQGGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
Qy 61 CTBPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCASVADTRCGCKPG 120
Db 61 CTBPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCASVADTRCGCKPG 120
Qy 121 WFEVCQVSCVSSPFYQCPLDCGALHRRHRLLCSSRDTCGTCLPGFYEHGDCVSCP 180
Db 121 WFEVCQVSCVSSPFYQCPLDCGALHRRHRLLCSSRDTCGTCLPGFYEHGDCVSCP 180

Qy 181 TSTLSCPERCAAVCGWRQMFVQVLLAGLVVPLLGATLTYYRHCWPHKPLVTADEAG 240
Db 181 TSTLSCPERCAAVCGWRQMFVQVLLAGLVVPLLGATLTYYRHCWPHKPLVTADEAG 240
Qy 241 MEALTTPPPATHSLPDSANTLLAPPDSSEKICTVQVLGNSWTFPGYPTQALCPQVTWSW 300
Db 241 MEALTTPPPATHSLPDSANTLLAPPDSSEKICTVQVLGNSWTFPGYPTQALCPQVTWSW 300
Qy 301 DQLPSPALGPAAPATLSPSPAGSPAMMLQPGQPLQDYVMDVAVPARRWKEFVRTLGLREAE 360
Db 301 DQLPSPALGPAAPATLSPSPAGSPAMMLQPGQPLQDYVMDVAVPARRWKEFVRTLGLREAE 360
Qy 361 IEAVEVEIGRFRDQOQYEMLKRWRQOQAGLGAVYAALERMGLDGCVEDLRSRLQRP 417
Db 361 IEAVEVEIGRFRDQOQYEMLKRWRQOQAGLGAVYAALERMGLDGCVEDLRSRLQRP 417

RESULT 5

US-11-174-467-1
; Sequence 1, Application US/11174467
; Publication No. US20060041106A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-3 POLYPEPTIDE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/174,467
; FILING DATE: 06-Jul-2005
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,069
; FILING DATE: 11-Sep-1997
; APPLICATION NUMBER: 60/026943
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1052R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-11-174-467-1

Query Match 45.2%; Score 1051; DB 7; Length 181;
Best Local Similarity 100.0%; Pred. No. 8.5e-76;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEQPRGCAVAALVLLGARAQGGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
Db 1 MEQPRGCAVAALVLLGARAQGGTSPRCDCAGDFHKKI GLFCRCGCPAGHYLKAP 60
Qy 61 CTBPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCASVADTRCGCKPG 120
Db 61 CTBPCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCASVADTRCGCKPG 120

QY 121 WFVECVQVSSSPFYCQCLDCGALHRRHTRLLCSRRDTCGTCCLPGFYEHGDCVSCP 180
Db 121 WFVECVQVSSSPFYCQCLDCGALHRRHTRLLCSRRDTCGTCCLPGFYEHGDCVSCP 180

QY 181 T 181
Db 181 T 181

RESULT 6

US-11-116-746-15
; Sequence 15, Application US/11116746
; Publication No. US20060020114A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin
; APPLICANT: Gurney, Austin
; APPLICANT: Wood, William
; TITLE OF INVENTION: Apo-2Dcr
; FILE REFERENCE: P1110
; CURRENT APPLICATION NUMBER: US/11/116,746
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/08/878,168
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 15
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-116-746-15

Query Match 16.4%; Score 381; DB 7; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.5e-23;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 338 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWRQOQAPGLGAVYAAL 397
Db 1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWRQOQAPGLGAVYAAL 60
QY 398 ERMGLDGCVEDLRS 411
Db 61 ERMGLDGCVEDLRS 74
RESULT 7
US-11-076-187-4
; Sequence 4, Application US/11076187
; Publication No. US20050244857A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Pan, James G
; APPLICANT: Gentz, Reiner L
; APPLICANT: Dixit, Vishva M
; TITLE OF INVENTION: Death Domain Containing Receptor-4
; FILE REFERENCE: PF35EP3
; CURRENT APPLICATION NUMBER: US/11/076,187
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: 60/035,722
; PRIOR FILING DATE: 1997-01-28
; PRIOR APPLICATION NUMBER: 60/037,829
; PRIOR FILING DATE: 1997-02-05
; PRIOR APPLICATION NUMBER: 09/013,895
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/132,922
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 09/565,918
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/406,922
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/413,861
; PRIOR FILING DATE: 2002-09-27

; PRIOR APPLICATION NUMBER: 10/648,786
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 60/551,768
; PRIOR FILING DATE: 2004-03-11
; PRIOR APPLICATION NUMBER: 60/608,469
; PRIOR FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 909
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-076-187-4

Query Match 16.1%; Score 374.5; DB 7; Length 909;
Best Local Similarity 28.5%; Pred. No. 7.6e-22;
Matches 132; Conservative 49; Mismatches 181; Indels 101; Gaps 23;
QY 15 LLLVLLGARAQG-----GTRSPR---CDCAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63
Db 14 LLELLVGIYPSGVIGLVPHLGDREKDSVCPQGYIHPQNNNSICCTKCHKGTLYLNDCPG 73
QY 64 PCGNSTCLVCPQDTFLAWENHNHSECARCOACDEQASQVALENCASAVADTRCGCKPGWVF 123
Db 74 P-GDITDCRECESGSFTASENHLR-HCLSCSKCKEMGQVEISSCTVDRTVCGCRKNQYR 131
QY 124 EC---QVSCVSSSPFYCQCLDCGALHRRHTRLLCSRRDTCGTCCLPGFYEHGDCVSCP 180
Db 132 HYWSENLFQC-----FNCSLCLN-GTVH-----LSCQEKQNTVCTCHAGFFLRENECVSC- 180
QY 181 TSTLGSQCPB--RCAAVC-----GWRQMFVQVLLAGLVPLLIGATITTYRHH 226
Db 181 ----SNCKSLEKTKLCLEQIENVKGTEDSGTIVLLPLVIFFGCLLSLLFGLMYRQYR 236
QY 227 CWPBK-----PLVTADKAMEALTPPPATHLSPLDS-----AHTLLAPDSSSEKIC 272
Db 237 -WKSLEYIVCGKSTPEKEGELEGTTKP---LAPNPSFSPSTPGFTPTLGFSPVPSSTFT 292
QY 273 TVOLVGNSTWTPGYPETEALCPQVTSWDOLPSRALGP-----AAAPTLSL- 318
Db 293 S-----SSTYTPGD-----CPNFA-----APREVAPPYQGDAPILATLASDIPNPL 336
QY 319 ---ESPAGSPAMMLQPGP-QLYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FRD 373
Db 337 QKWEDSAHKPQSLDTPDPAFLYAVENVPLRWKEFVRRLGLSDHEIDRLQLNGRCLRE 396
QY 374 QQYEMLKRWRQOQP---AGLGAVYAALERMGLDGCVEDLRSRL 413
Db 397 AQYSLATWRRRTPRREATLELIGRVLRDMDLIGCLEDEAL 439

RESULT 8

US-11-182-946-3
; Sequence 3, Application US/11182946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 455
; TYPE: PRT

ORGANISM: Homo sapiens
US-11-182-946-3

Query Match 16.1%; Score 374; DB 7; Length 455;
Best Local Similarity 28.3%; Pred. No. 3.9e-22;
Matches 131; Conservative 49; Mismatches 183; Indels 100; Gaps 22;
QY 15 LLLVLLGARAQG-----GTRSPR---CDCAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63
DB 15 LLELLVGYPSGIVGLPHLGDREKDSVCPQGIHPQNNISICTCKHGTLYLNDPCG 74
QY 64 PCGNTCLVCPDPTFLAMNHNSECARCOACDEQASQVALENCASAVADTRCGCKPGWVFV 123
DB 75 PQQDTCRECSGSFTASENHLR-HCLSCSKCKEMGQVEISSCTVDRDTCVCGCRKQYR 133
QY 124 EC---QVSCVSSSPYQPCDCCALHRRHLLCSRRTDCGTCCLPGFYEHDGCVSCP 180
DB 134 HYWSENLFQC-----FNCSLCLN-GTVH-----LSCQEKQNTVCTCHAGFFLRENECVSC- 182
QY 181 TSTLSCPE--RCAAVC-----GWRQMFVQVLLAGLVVPLLGLATLTYTRH 226
DB 183 ----SNCKSLECKLCLPQIENVKGTEDSGTTVLLPLVIFGLCLLSLLFGLMYRYQR 238
QY 227 CWPBK-----PLVTADAGMEALTPPPATHLSPLDS-----AHTLLAPDSEKIC 272
DB 239 -WKSXYIVSCGKSTPEKEGLEGTTKP---LAPNPSPTPGFTPLGSPVPSSTFT 294
QY 273 TVQLVGNSTWPGYETQALCPQVTSWDQLPSRALGP-----AAAPTLS- 318
DB 295 S-----SSTYTPGD-----CPNFA-----APREVAPPYQADPILATALASDPIPNPL 338
QY 319 ---ESPAGSPAMMLQBP-QLYDMDVAPARWKEFVRTGLREABIEAVEVEIGR-FRD 373
DB 339 QKWESAHKPSQLDTPDPA TLVAVENVPLRWKEFVRRLGLSDHEIDRLQNGRCLRE 398
QY 374 QOYEMLKRWROQP---AGLGAVYAALERMGLDGCVEDLRSL 413
DB 399 AQYSMLATWRRTPREATLELLGRVLRDMDLLGCLDIEEAL 441

RESULT 9

US-11-185-878-5
; Sequence 5, Application US/11185878
; Publication No. US20050282217A1
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Rosen, Craig A
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor 10
; FILE REFERENCE: PF379P1D1
; CURRENT APPLICATION NUMBER: US/11/185,878
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/280,047
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 09/580,212
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/086,483
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/069,112
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: 60/050,936
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/144,023
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: 60/142,563
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: 60/136,786
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; TYPE: PRT
; ORGANISM: human

US-11-185-878-5

Query Match 15.7%; Score 364.5; DB 7; Length 453;
Best Local Similarity 28.2%; Pred. No. 2.2e-21;
Matches 126; Conservative 50; Mismatches 178; Indels 93; Gaps 21;
QY 20 LGARAQGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAPCTEPCGNTCLVCPDTPFL 79
DB 33 LGDREKDSVCPQ---GKYIHPNNSICTCKHGTLYLNDPCGQDTCRECSGSFT 88
QY 80 AWENHNSECARCOACDEQASQVALENCASAVADTRCGCKPGWVFEC---QVSCVSSSP 136
DB 89 ASENHLR-HCLSCSKCKEMGQVEISSCTVDRDTCVCGCRKQYRYWSENLFQC-----F 142
QY 137 YCQPCDCCALHRRHLLCSRRTDCGTCCLPGFYEHDGCVSCPSTLGSCE--RCAAV 194
DB 143 NCSLCLN-GTVH-----LSCQEKQNTVCTCHAGFFLRENECVSC-----SNCKSLECKL 192
QY 195 C-----GWRQMFVQVLLAGLVVPLLGLATLTYTRHWPBK-----PLVT 235
DB 193 CLPQIENVKGTEDSGTTVLLPLVIFGLCLLSLLFGLMYRYQR-WKSXYIVSCGKSTP 251
QY 236 ADEAGMEALTPPPATHLSPLDS-----AHTLLAPDSEKICITVQLVGNSTWPGYETP 288
DB 252 EKEGLEGTTKP---LAPNPSPTPGFTPLGSPVPSSTFTS-----SSTYTPGD--- 301
QY 289 QEALCPQVTSWDQLPSRALGP-----AAAPTLS-ESPAGSPAMMLQBP 331
DB 302 ----CPNFA-----APREVAPPYQADPILATALASDPIPNLQKWESAHKPSQLDTP 352
QY 332 GP-QLYDMDVAPARWKEFVRTGLREABIEAVEVEIGR-FRDQOYEMLKRWROQP--- 387
DB 353 DPATLYAVENVPLRWKEFVRRLGLSDHEIDRLQNGRCLREAQYSMLATWRRTPRR 412
QY 388 -AGLGAVYAALERMGLDGCVEDLRSL 413
DB 413 EATLELLGRVLRDMDLLGCLDIEEAL 439

RESULT 10

US-10-987-663-4
; Sequence 4, Application US/10987663
; Publication No. US20050272118A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: CLARK, HILARY
; APPLICANT: EATON, DANIEL L.
; APPLICANT: WRANIK, BERND
; APPLICANT: OUYANG, WENJUN
; APPLICANT: GONZALES, LINO
; APPLICANT: LOYET, KELLY M.
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of
; TITLE OF INVENTION: Immune Related Diseases
; FILE REFERENCE: P1996R1P1-US
; CURRENT APPLICATION NUMBER: US/10/987,663-
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 60/421,236
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 10/371,341
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-987-663-4

Query Match 8.9%; Score 206.5; DB 6; Length 283;
Best Local Similarity 27.4%; Pred. No. 3.4e-09;
Matches 74; Conservative 28; Mismatches 119; Indels 49; Gaps 13;
QY 15 LLLVLLGARAQGTSPRCDCAGDFHKKIGLFCRCGCPAGHYLKAPCTEPCGNTCLVCP 74

Db 25 LYLTFLGAPCY----APALPSCKEDEYPVGECCPKCSPGYRVKEACGELTG-TVCEPCP 79
QY 75 QDTFLAWENHN--SECARCOAQDEQASQVALENCASAVADTRCGCKPGWVEQVQSOCVS 132
Db 80 PGYIIA---HNLGSLCKLQCMCDPAMGLRASRNCSTENAVCGCSPGHF-----CIV 129
QY 133 SSPFYQPCPLDCGALHRRHRL--CSRRDTCGTCLPGFYEHGDCGVCSPSTLGSQCP 189
Db 130 QGDHCAACRAYATSSPGQVKGTTESQDTLQNCPPGTF-----PNTLEECQH 181
QY 190 --RCA-----AVCGWRQMFVVQVLLAGLVPLLLGAT--LTYTYRHCVHP-----KPLVTA 236
Db 182 QTRCSMLVTRKAGAGTSSSHVWVWFLSGSLVIVIVCVSTVGLIICVGRKPRGDVVKIVSV 241
QY 237 DEAGMEALTPPPATHLSPLDSANTLAPPD 266
Db 242 QRKRQEA--EGEATVIEALQ-----APPD 263

RESULT 11
US-11-126-126-2
; Sequence 2, Application US/11126126
; Publication No. US20050250696A1
; GENERAL INFORMATION:
; APPLICANT: Fisher F., Eric
; APPLICANT: Edwards K., Carl
; APPLICANT: Kieft L., Gary
; TITLE OF INVENTION: Truncated Soluble Tumor Necrosis Factor Type-I and
; FILE OF INVENTION: Type-II Receptors
; FILE REFERENCE: 02-006-A
; CURRENT APPLICATION NUMBER: US/11/126,126
; PRIOR FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: 09/882,735
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/214,613
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: 09/12244
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: 60/039,792
; PRIOR FILING DATE: 1997-03-04
; PRIOR APPLICATION NUMBER: 60/039,314
; PRIOR FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: 60/037,737
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: 60/032,534
; PRIOR FILING DATE: 1996-12-06
; PRIOR APPLICATION NUMBER: 60/021,443
; PRIOR FILING DATE: 1996-07-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-126-126-2

Query Match 8.6%; Score 200.5; DB 7; Length 161;
Best Local Similarity 29.8%; Pred. No. 5.5e-09;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
QY 40 HKKIGLFCRCGCPAGHYLKAPCTPCGNSCLVCPQDTFLAWENHNSECARCOAQDEQA 99
Db 11 HPQNNISCTCKHKGYLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKEM 69
QY 100 SQVALENCASAVADTRCGCKPGWFEVC---QVSCVSSSPFYQPCPLDCGALHRRHRLCS 156
Db 70 GQVEISSCTVDRDTVCGCRKNQRYHWSNLFC-----FNCSCLN-GTVH---LSCQ 119
QY 157 RRDTCGTCLPGFYEHGDCGVCSPSTLGSQCP--RCAAVC 195
Db 120 EKQNTVCTCHAGFFLENECVSC-----SNCKKSLCTKLC 155

RESULT 12
US-11-057-923-3
; Sequence 3, Application US/11057923
; Publication No. US20050287152A1
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; APPLICANT: Khare, Sanjay D.
; APPLICANT: Keige, Ulrich
; TITLE OF INVENTION: COMPOSITIONS AND METHODS TO MODULATE AN IMMUNE RESPONSE TO AN
; FILE OF INVENTION: IMMUNOGENIC THERAPEUTIC AGENT
; FILE REFERENCE: 54113.8008.WO00
; CURRENT APPLICATION NUMBER: US/11/057,923
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: PCT/US04/35415
; PRIOR FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: US 60/515,199
; PRIOR FILING DATE: 2003-10-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: 30kDa TNF Inhibitor
US-11-057-923-3

Query Match 8.6%; Score 200.5; DB 7; Length 161;
Best Local Similarity 29.8%; Pred. No. 5.5e-09;
Matches 48; Conservative 20; Mismatches 72; Indels 21; Gaps 7;
QY 40 HKKIGLFCRCGCPAGHYLKAPCTPCGNSCLVCPQDTFLAWENHNSECARCOAQDEQA 99
Db 11 HPQNNISCTCKHKGYLYNDPCPGQDTCRECSGSFTASENHLR-HCLSCSKCKEM 69
QY 100 SQVALENCASAVADTRCGCKPGWFEVC---QVSCVSSSPFYQPCPLDCGALHRRHRLCS 156
Db 70 GQVEISSCTVDRDTVCGCRKNQRYHWSNLFC-----FNCSCLN-GTVH---LSCQ 119
QY 157 RRDTCGTCLPGFYEHGDCGVCSPSTLGSQCP--RCAAVC 195
Db 120 EKQNTVCTCHAGFFLENECVSC-----SNCKKSLCTKLC 155

RESULT 13
US-11-182-946-7
; Sequence 7, Application US/11182946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Pei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-946-7

Query Match 8.6%; Score 199.5; DB 7; Length 335;
Best Local Similarity 21.4%; Pred. No. 1.5e-08;
Matches 74; Conservative 43; Mismatches 106; Indels 123; Gaps 12;

QY 44 GLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARCAQCADEQASQVA 103
Db 56 GQFCHKPCPPGKARDCTVNGDEPDCVPQCGKEYTDKAHFSKRCRLCDEGHGLEV 115
QY 104 LENCASAVADTRCGCKPGWFEVCQVSCVSSPPYCPCLDCCGALHRRHLLCSRRTDCG 163
Db 116 EINCTRTQNTKCRCKNFF-----CNSTVCEHCDPCTKC----- 149
QY 164 TCLPGFYHGDGCVSCTSTLSCPCERCAAVCGWR-QMFWVQVLLAGLVVPLLGLATLY 222
Db 150 -----EHGI-1KECTLTSTNTCKEE-----GSRNLGWLCLLL-LPLILVWVRKE 194
QY 223 TYRHCHWPHKPLVTADAGMEALTPPPTHLSPLDSAHTL---LAPDSEKICTVOLVGN 279
Db 195 VQKTCRKR-----KENQG-----SHESPTLNPTETVAINLSVDLSKYITI----- 236
QY 280 SWTPGYPTEQALCPQVTSWDLPSRALGPAAPTLSPESPAGSPAMMLQPGPQLYDVM 339
Db 237 -----AGVMTLS----- 243
QY 340 DAVPARRWKEFVRTLGLREAEIEAVEVE-IGRFRDQOQYEMLKWRQ 384
Db 244 -----QVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNWHQ 283

RESULT 14

US-11-076-187-3

; Sequence 3, Application US/11076187

; Publication No. US20050244857A1

; GENERAL INFORMATION:

; APPLICANT: Ni, Jian

; APPLICANT: Rosen, Craig A

; APPLICANT: Pan, James G

; APPLICANT: Gentz, Reiner L

; APPLICANT: Dixit, Vishva M

; TITLE OF INVENTION: Death Domain Containing Receptor-4

; FILE REFERENCE: PF355P3

; CURRENT APPLICATION NUMBER: US/11/076,187

; CURRENT FILING DATE: 2005-03-10

; PRIOR APPLICATION NUMBER: 60/035,722

; PRIOR FILING DATE: 1997-01-28

; PRIOR APPLICATION NUMBER: 60/037,829

; PRIOR FILING DATE: 1997-02-05

; PRIOR APPLICATION NUMBER: 09/013,895

; PRIOR FILING DATE: 1998-01-27

; PRIOR APPLICATION NUMBER: 60/132,922

; PRIOR FILING DATE: 1999-05-06

; PRIOR APPLICATION NUMBER: 09/565,918

; PRIOR FILING DATE: 2000-05-05

; PRIOR APPLICATION NUMBER: 60/406,922

; PRIOR FILING DATE: 2002-08-30

; PRIOR APPLICATION NUMBER: 60/413,861

; PRIOR FILING DATE: 2002-09-27

; PRIOR APPLICATION NUMBER: 10/648,786

; PRIOR FILING DATE: 2003-08-27

; PRIOR APPLICATION NUMBER: 60/551,768

; PRIOR FILING DATE: 2004-03-11

; PRIOR APPLICATION NUMBER: 60/608,469

; PRIOR FILING DATE: 2004-09-10

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 3

; LENGTH: 669

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-076-187-3

Query Match 8.6%; Score 199.5; DB 7; Length 669;

Best Local Similarity 21.4%; Pred. No. 3.1e-08;

Matches 74; Conservative 43; Mismatches 106; Indels 123; Gaps 12;

QY 44 GLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARCAQCADEQASQVA 103

Db 56 GQFCHKPCPPGKARDCTVNGDEPDCVPQCGKEYTDKAHFSKRCRLCDEGHGLEV 115
QY 104 LENCASAVADTRCGCKPGWFEVCQVSCVSSPPYCPCLDCCGALHRRHLLCSRRTDCG 163
Db 116 EINCTRTQNTKCRCKNFF-----CNSTVCEHCDPCTKC----- 149
QY 164 TCLPGFYHGDGCVSCTSTLSCPCERCAAVCGWR-QMFWVQVLLAGLVVPLLGLATLY 222
Db 150 -----EHGI-1KECTLTSTNTCKEE-----GSRNLGWLCLLL-LPLILVWVRKE 194
QY 223 TYRHCHWPHKPLVTADAGMEALTPPPTHLSPLDSAHTL---LAPDSEKICTVOLVGN 279
Db 195 VQKTCRKR-----KENQG-----SHESPTLNPTETVAINLSVDLSKYITI----- 236
QY 280 SWTPGYPTEQALCPQVTSWDLPSRALGPAAPTLSPESPAGSPAMMLQPGPQLYDVM 339
Db 237 -----AGVMTLS----- 243
QY 340 DAVPARRWKEFVRTLGLREAEIEAVEVE-IGRFRDQOQYEMLKWRQ 384
Db 244 -----QVKGFRKNGVNEAKIDEIKNDNVQDTAEQKVOLLRNWHQ 283

RESULT 15

US-11-185-878-3

; Sequence 3, Application US/11185878

; Publication No. US20050282217A1

; GENERAL INFORMATION:

; APPLICANT: Ni, Jian

; APPLICANT: Rosen, Craig A

; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor 10

; FILE REFERENCE: PF379PID1

; CURRENT APPLICATION NUMBER: US/11/185,878

; CURRENT FILING DATE: 2005-07-21

; PRIOR APPLICATION NUMBER: US/10/280,047

; PRIOR FILING DATE: 2002-10-25

; PRIOR APPLICATION NUMBER: 09/580,212

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 09/086,483

; PRIOR FILING DATE: 1998-05-29

; PRIOR APPLICATION NUMBER: 60/069,112

; PRIOR FILING DATE: 1997-12-09

; PRIOR APPLICATION NUMBER: 60/050,936

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/144,023

; PRIOR FILING DATE: 1999-07-15

; PRIOR APPLICATION NUMBER: 60/142,563

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: 60/136,786

; PRIOR FILING DATE: 1999-05-28

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 331

; TYPE: PRT

; ORGANISM: human

US-11-185-878-3

Query Match 8.5%; Score 197; DB 7; Length 331;

Best Local Similarity 21.1%; Pred. No. 2.3e-08;

Matches 72; Conservative 41; Mismatches 106; Indels 122; Gaps 11;

QY 48 CRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLAWENHNSECARCAQCADEQASQVALENC 107
Db 58 CHPCPPGKARDCTVNGDEPDCVPQCGKEYTDKAHFSKRCRLCDEGHGLEVINC 117
QY 108 SAVADTRCGCKPGWFEVCQVSCVSSPPYCPCLDCCGALHRRHLLCSRRTDCGTCPLP 167
Db 118 TRQNTKCRCKNFF-----CNSTVCEHCDPCTKC----- 147
QY 168 GFVEHGDGCVSCTSTLSCPCERCAAVCGWRQMFVQVLLAGLVVPLLGLATLYTYRHC 227

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Db      148  ---EHGI-IKECTLTSTNKCEE-----GSRNGWLCLLL--LPIPLIVWYKREVKQTC 196
Qy      228  WPHKPLVTADAGMEALTPPPATHLSPLDSAHTL---LAPDSSEKICTVQLVGNWTPG 284
Db      197  RKHR-----KENQG-----SHESTLNPETVAINLSDDVLSKYITTI----- 233
Qy      285  YPETQALCPQVTVSWDQPSRALGPAAAPTLSPESPAGSPAMMLQPGPOLYDVMDAVPA 344
Db      234  -----AGVMTLS----- 240
Qy      345  RRWKEFVRTLGLREAEIEAVEVE-IGRFRDOQYEMLKRWQ 384
Db      241  -QVKGFRKNGVNEAKIDEIKNDNVQDTAEQVQLLRNHQ 280

```

Search completed: March 20, 2006, 08:01:30
 Job time : 29 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 08:03:29 ; Search time 25 Seconds
(without alignments)
264.562 Million cell updates/sec

Title: US-10-081-280-6_COPY_338_417

Perfect score: 413

Sequence: 1 VMDVAPRRKFEVRLGLR.....ERMGLDCCVEDLRSLRQGP 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 345832

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCUTS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	338	81.8	65	2	US-09-527-236A-24
2	338	81.8	65	2	US-09-756-854-24
3	338	81.8	65	2	US-10-041-574-24
4	338	81.8	65	2	US-09-095-094-24
5	155	37.5	78	2	US-08-828-683A-23
6	142	34.4	70	2	US-09-159-277A-6
7	142	34.4	70	2	US-08-844-691A-6
8	136.5	33.1	68	2	US-09-527-236A-23
9	136.5	33.1	68	2	US-09-756-854-23
10	136.5	33.1	68	2	US-10-041-574-23
11	136.5	33.1	68	2	US-09-095-094-23
12	118	28.6	64	2	US-08-894-626-3
13	102.5	24.8	45	1	US-08-219-237B-11
14	83	20.1	67	2	US-09-527-236A-26
15	83	20.1	67	2	US-09-756-854-26
16	83	20.1	67	2	US-10-041-574-26
17	83	20.1	67	2	US-09-095-094-26
18	73.5	17.8	41	1	US-08-444-005-28
19	70.5	17.1	77	2	US-08-995-159-7
20	70.5	17.1	77	2	US-08-828-683A-27
21	70.5	17.1	77	2	US-09-545-605-7
22	70.5	17.1	77	2	US-09-056-383-1
23	68	16.5	40	1	US-08-444-005-22
24	68	16.5	40	1	US-09-527-236A-25
25	68	16.5	67	2	US-09-756-854-25
26	68	16.5	67	2	US-10-041-574-25
27	68	16.5	67	2	US-09-095-094-25

28 67 16.2 41 1 US-08-444-005-23 Sequence 23, Appl
29 67 16.2 51 2 US-08-883-036A-4 Sequence 4, Appl
30 67 16.2 51 2 US-09-536-201-4 Sequence 4, Appl
31 67 16.2 51 2 US-09-578-392-4 Sequence 4, Appl
32 65.5 15.9 41 1 US-08-444-005-29 Sequence 29, Appl
33 60 14.5 77 2 US-09-069-827A-118 Sequence 118, Appl
34 59 14.3 68 2 US-08-995-050-1 Sequence 1, Appl
35 57.5 13.9 45 1 US-08-219-237B-10 Sequence 10, Appl
36 57.5 13.9 63 2 US-08-894-626-1 Sequence 10, Appl
37 57.5 13.9 68 2 US-09-527-236A-22 Sequence 22, Appl
38 57.5 13.9 68 2 US-09-756-854-22 Sequence 22, Appl
39 57.5 13.9 68 2 US-10-041-574-22 Sequence 22, Appl
40 57.5 13.9 68 2 US-09-095-094-22 Sequence 22, Appl
41 57.5 13.9 70 2 US-09-159-277A-5 Sequence 5, Appl
42 57.5 13.9 70 2 US-08-844-691A-5 Sequence 5, Appl
43 57.5 13.9 77 2 US-08-828-683A-24 Sequence 24, Appl
44 54.5 13.2 63 2 US-08-894-626-2 Sequence 2, Appl
45 54 13.1 25 1 US-08-580-988A-27 Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-09-527-236A-24
; Sequence 24, Application US/09527236A
; Patent No. 6358508
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/09/527,236A
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-527-236A-24

Query Match 81.8% Score 338; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 66-37;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 RWKEFVRLGLRRAEIAEVEIGRFDQYQYEMLRKWRQQQAGLGAVYAALERMGLDGC 68
Db 1 RWKEFVRLGLRRAEIAEVEIGRFDQYQYEMLRKWRQQQAGLGAVYAALERMGLDGC 60

RESULT 2
US-09-756-854-24
; Sequence 24, Application US/09756854
; Patent No. 6667390
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping

Qy 69 VEDLR 73
Db 61 VEDLR 65

RESULT 5

US-08-828-683A-23
; Sequence 23, Application US/08828683A
; Patent No. 6469144
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 78 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-08-828-683A-23

Query Match 37.5%; Score 155; DB 2; Length 78;
Best Local Similarity 46.1%; Pred. No. 8.1e-13;
Matches 35; Conservative 13; Mismatches 24; Indels 4; Gaps 2;

Qy 1 VMDAVPARRKKEFVRLGLREARIEAVEVEIGR-FRDOQYEMLKRWQOOP---AGLGAV 56
Db 1 WVENVPLRWKEFVRLGLSDHEIDRLONGRCLEAQSMLATWRRRTPREATLELL 60

Qy 57 YAALERMLDGCVDL 72
Db 61 GRVLRMDLLGCLEDI 76

RESULT 6

US-09-159-277A-6
; Sequence 6, Application US/09159277A
; Patent No. 6562797
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: O'ROURKE, KAREN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING
; TITLE OF INVENTION: FAS-ASSOCIATED APOPTOSIS
; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/159,277A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,691
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: US 08/416,379
; FILING DATE: 03-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Koneki, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442107001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)813-5600
; TELEFAX: (650)494-0792
; TELEX: 706141 MESNFOERS SFO
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 70 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /note= "Leu is replaced by Asn for
; OTHER INFORMATION: the point mutant hTNR-1"
US-09-159-277A-6

Query Match 34.4%; Score 142; DB 2; Length 70;
Best Local Similarity 47.1%; Pred. No. 3.6e-11;
Matches 32; Conservative 11; Mismatches 21; Indels 4; Gaps 2;

Qy 9 RWKEFVRLGLREARIEAVEVEIGR-FRDOQYEMLKRWQOOP---AGLGAVYALERMG 64
Db 1 RWKEFVRLGLSDHEIDRLONGRCLEAQSMLATWRRRTPREATLELLGRVLRMD 60

Qy 65 LDGCVDL 72
Db 61 LLGCLEDI 68

RESULT 7

US-08-844-691A-6
; Sequence 6, Application US/08844691A
; Patent No. 6747138
; GENERAL INFORMATION:
; APPLICANT: DIXIT, VISHVA M.
; APPLICANT: O'ROURKE, KAREN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING
; TITLE OF INVENTION: FAS-ASSOCIATED APOPTOSIS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018

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Db 61 LGCLEDI 67

RESULT 10

US-10-041-574-23
; Sequence 23, Application US/10041574

; Patent No. 6919078

; GENERAL INFORMATION:

; APPLICANT: Ni, Jian

; APPLICANT: Yu, Guo-Liang

; APPLICANT: Fan, Ping

; APPLICANT: Gentz, Reiner L.

; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9

; FILE REFERENCE: PF375P1

; CURRENT APPLICATION NUMBER: US/10/041,574

; CURRENT FILING DATE: 2002-01-10

; PRIOR APPLICATION NUMBER: 09/527,236

; PRIOR FILING DATE: 2000-03-16

; PRIOR APPLICATION NUMBER: 60/052,991

; PRIOR FILING DATE: 1997-06-11

; PRIOR APPLICATION NUMBER: 09/095,094

; PRIOR FILING DATE: 1998-06-10

; PRIOR APPLICATION NUMBER: 60/126,019

; PRIOR FILING DATE: 1999-03-24

; PRIOR APPLICATION NUMBER: 60/134,220

; PRIOR FILING DATE: 1999-05-14

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 23

; LENGTH: 68

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-041-574-23

Query Match

Best Local Similarity 33.1%; Score 136.5; DB 2; Length 68;

Matches 31; Conservative 12; Mismatches 21; Indels 3; Gaps 2;

QY 9 RWKEFVRTGLREAEIENAVEVEIGR-PRDOQYEMLKWRQ--QQPAGLGAVYAALERMGL 65

Db 1 RWKEFVRTGLSDHEIDRLQNGRCLEAQAQYSLATWRRRTREATLELLGRVLRDMDL 60

QY 66 DGCVEDL 72

Db 61 LGCLEDI 67

RESULT 11

US-09-095-094-23

; Sequence 23, Application US/09095094

; Patent No. 6949358

; GENERAL INFORMATION:

; APPLICANT: Ni, Jian

; APPLICANT: Yu, Guo-Liang

; APPLICANT: Fan, Ping

; APPLICANT: Gentz, Reiner

; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: US

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/095,094

; FILING DATE:

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley K.
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF375
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-095-094-23

Query Match 33.1%; Score 136.5; DB 2; Length 68;
Best Local Similarity 46.3%; Pred. No. 1.8e-10;
Matches 31; Conservative 12; Mismatches 21; Indels 3; Gaps 2;

QY 9 RWKEFVRTGLREAEIENAVEVEIGR-PRDOQYEMLKWRQ--QQPAGLGAVYAALERMGL 65

Db 1 RWKEFVRTGLSDHEIDRLQNGRCLEAQAQYSLATWRRRTREATLELLGRVLRDMDL 60

QY 66 DGCVEDL 72

Db 61 LGCLEDI 67

RESULT 12

US-08-894-626-3

; Sequence 3, Application US/08894626

; Patent No. 6355780

; GENERAL INFORMATION:

; APPLICANT: WALLACH, David

; BOLDIN, Mark P.

; VARGOLOMEV, Eugene E.

; PANCER, Zeev

; METT, Igor

; GONCHAROV, Tanya M.

; WEINWURZEL, Henry

; TITLE OF INVENTION: MODULATORS OF REGULATORY PROTEINS

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.

; STREET: 419 Seventh Street N.W., Ste. 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/894,626

; FILING DATE: 09-Dec-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: IL 112,742

; FILING DATE: 22-FEB-1995

; APPLICATION NUMBER: IL 115,289

; FILING DATE: 13-SEP-1995

; APPLICATION NUMBER: PCT/US96/02326

; FILING DATE: 15-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: BROWDY, Roger L.

; REGISTRATION NUMBER: 25,618

; REFERENCE/DOCKET NUMBER: WALLACH-17

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 628-5197

; TELEFAX: (202) 737-3528

Mon Mar 20 08:26:42 2006

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 64 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-08-894-626-3
 Query Match 28.6%; Score 118; DB 2; Length 64;
 Best Local Similarity 42.6%; Pred. No. 4.5e-08;
 Matches 29; Conservative 10; Mismatches 17; Indels 12; Gaps 3;
 QY 10 WKFEVRLGLREAEIEAVEVEIGR-FRDOQYEMLKRWQOOPAGLGVVAALERMG---64
 DB 1 WKFEVRLGLSDHEIDRLQNGRCLEAQSMLATWRRTPRR-----EATLELGRVLR 56
 QY 65 ---LDGCV 69
 DB 57 DHDLGLCL 64

RESULT 13
 US-08-219-237B-11
 ; Sequence 11, Application US/08219237B
 ; Patent No. 5674546
 ; GENERAL INFORMATION:
 ; APPLICANT: NAGATA, Shigekazu
 ; APPLICANT: ITOH, Naoto
 ; APPLICANT: YONEHARA, Shin
 ; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: James W. Hellwege
 ; STREET: P.O. Box 2266 Bads Station
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: USA
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION NUMBER: US/08/219,237B
 ; FILING DATE: 28-MAR-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/872,129
 ; FILING DATE: 22-APR-1992
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: James W. Hellwege
 ; REGISTRATION NUMBER: 28,808
 ; REFERENCE/DOCKET NUMBER: 516762
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 45 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-219-237B-11

Query Match 24.8%; Score 102.5; DB 1; Length 45;
 Best Local Similarity 51.2%; Pred. No. 3.1e-06;
 Matches 21; Conservative 8; Mismatches 11; Indels 1; Gaps 1;
 QY 11 KEFVRLGLREAEIEAVEVEIGR-FRDOQYEMLKRWQOOP 50
 DB 1 KEFVRLGLSDHEIDRLQNGRCLEAQSMLATWRRTP 41

RESULT 14
 US-09-527-236A-26
 ; Sequence 26, Application US/09527236A
 ; Patent No. 6358508
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Fan, Ping
 ; APPLICANT: Gentz, Reiner L.
 ; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
 ; FILE REFERENCE: PF375P1
 ; CURRENT APPLICATION NUMBER: US/09/527,236A
 ; CURRENT FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/052,991
 ; PRIOR FILING DATE: 1997-06-11
 ; PRIOR APPLICATION NUMBER: 09/095,094
 ; PRIOR FILING DATE: 1998-06-10
 ; PRIOR APPLICATION NUMBER: 60/126,019
 ; PRIOR FILING DATE: 1999-03-24
 ; PRIOR APPLICATION NUMBER: 60/134,220
 ; PRIOR FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 26
 ; LENGTH: 67
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-527-236A-26

Query Match 20.1%; Score 83; DB 2; Length 67;
 Best Local Similarity 33.3%; Pred. No. 0.0019;
 Matches 19; Conservative 11; Mismatches 25; Indels 2; Gaps 1;
 QY 10 WKFEVRLGLREAEIEAVEVEIGRFRDOQYEMLKRW--RQOOPAGLGVVAALERMG 64
 DB 2 WEPLMKLGLMDNEIKVAKAEAGHRDTLYTLIKWVNTKGRDASVHTLLDALETLG 58

RESULT 15
 US-09-756-854-26
 ; Sequence 26, Application US/09756854
 ; Patent No. 6667390
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Fan, Ping
 ; APPLICANT: Gentz, Reiner
 ; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: US
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION NUMBER: US/09/756,854
 ; FILING DATE: 10-Jan-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/095,094
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hoover, Kenley K.
 ; REGISTRATION NUMBER: 40,302
 ; REFERENCE/DOCKET NUMBER: PF375

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 67 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-756-854-26

Query Match 20.1%; Score 83; DB 2; Length 67;

Best Local Similarity 33.3%; Pred. No. 0.0019;

Matches 19; Conservative 11; Mismatches 25; Indels 2; Gaps 1;

Qy 10 WKPFVRLGLEAEIEAVEVEIGRFRDQOYEMLKRW--RQOQPACLGAVYAALERMG 64

Db 2 WEPLMRKLGMDNEIKVAKAEAGHRDLYTMTLIKWNKTRDASVHTLLDALETG 58

Search completed: March 20, 2006, 08:04:05

Job time : 25 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 08:03:18 ; Search time 23 Seconds
(without alignments)
334.667 Million cell updates/sec

Title: US-10-081-280-6_COPY_338_417

Perfect score: 413
Sequence: 1 VMDVPAARKKEFVTLGLR.....ERMGLDGCVEDLSRLQRP 80

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 26016

Minimum DB seq length: 0
Maximum DB seq length: 80

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52.5	12.7	74	2 F71080	hypothetical prote
2	50.5	12.2	71	2 G69463	conserved hypotet
3	50.5	12.2	72	2 E69386	hypothetical prote
4	50.5	12.2	73	2 D69499	conserved hypotet
5	50.5	12.2	79	2 A84092	hypothetical prote
6	49.5	12.0	78	2 H84353	hypothetical prote
7	48	11.6	72	2 A82881	conserved hypotet
8	47	11.4	60	2 D83610	hypothetical prote
9	47	11.4	61	2 C69333	hypothetical prote
10	47	11.4	67	2 A96702	unknown protein, 7
11	46.5	11.3	64	2 G83940	hypothetical prote
12	46.5	11.3	68	2 JH0129	repressor protein
13	46.5	11.3	79	2 AH0619	probable damage-in
14	46	11.1	72	2 A75099	hypothetical prote
15	46	11.1	76	2 H70576	hypothetical prote
16	45.5	11.0	52	2 F83985	hypothetical prote
17	45	10.9	67	2 AC1037	probable phage tai
18	45	10.9	71	2 F70799	integrase-related
19	45	10.9	80	2 F72303	glutaredoxin - The
20	44.5	10.8	72	2 G91153	host factor for ly
21	44.5	10.8	72	2 C85999	host factor for ly
22	44.5	10.8	72	2 A49988	slyx protein - Esc
23	44.5	10.8	74	2 B75199	hypothetical prote
24	44	10.7	67	2 AG0927	probable phage tai
25	44	10.7	68	2 B55682	keratin 15, type I
26	44	10.7	70	2 F81899	hypothetical prote
27	43.5	10.5	62	2 F69871	hypothetical prote
28	43.5	10.5	75	2 AE2659	conserved hypotet
29	43.5	10.5	75	2 C97441	hypothetical prote

30 43 10.4 65 2 E70644 probable ribosomal
31 43 10.4 65 2 A90826 lcd-like protein
32 43 10.4 65 2 H81238 hypothetical prote
33 43 10.4 71 2 T45384 ribosomal prote
34 43 10.4 73 2 F64547 hypothetical prote
35 43 10.4 77 2 F69219 conserved hypotet
36 42.5 10.3 47 2 I53270 mineralocorticoid
37 42.5 10.3 58 2 S60803 M protein precursor
38 42.5 10.3 77 2 A82086 hypothetical prote
39 42.5 10.3 79 2 F72592 hypothetical prote
40 42.5 10.3 80 2 S60835 M protein precursor
41 42 10.2 37 2 D69283 conserved hypotet
42 42 10.2 61 2 AD2769 hypothetical prote
43 42 10.2 73 2 H83960 hypothetical prote
44 42 10.2 77 2 D81212 50S ribosomal prot
45 41.5 10.0 36 2 C69327 hypothetical prote

ALIGNMENTS

RESULT 1

F71080

hypothetical protein PHS027 - Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii

C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004

C;Accession: F71080

R;Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,

DNA Res. 5, 55-76, 1998

A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A;Reference number: A71000; MUID:98344137; PMID:9679194

A;Accession: F71080

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-74 <XAW>

A;Cross-references: UNIPROT:O73992; UNIPARC:UPI0000062CAA; GB:AP000004; NID:93236131; PII

A;Experimental source: strain OT3

A;Note: this accession replaces an interim accession for a sequence replaced by GenBank

C;Genetics:

A;Gene: PHS027

Query Match 12.7%; Score 52.5; DB 2; Length 74;

Best Local Similarity 27.3%; Pred. No. 81;

Matches 18; Conservative 14; Mismatches 27; Indels 7; Gaps 2;

QY 5 VPARRKKEFVTLGLREARIEAVEVEIGRFRQQYEMLKRWQQQAGLGAAYAAERMG 64

DB 14 IFA----EIRKALGKGBLLEVLKEDGKI---IIRLKKRKTLLKGLKLTPEIEKAI 66

QY 65 LDGCVF 70

DB 67 VEGMKE 72

RESULT 2

G69463

conserved hypothetical protein AF1712 - Archaeoglobus fulgidus

C;Species: Archaeoglobus fulgidus

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: G69463

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.,

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.P.; McDonald, L.

Nature 390, 364-370, 1997

A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Ariach, P.; Kaine, B.P.; Sykes, S.N

Smith, H.O.; Woese, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: G69463

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-71 <KLE>


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unknown protein, 70659-70456 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: A96702
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.;
ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A96702
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-67 <STO>
A:Cross-references: UNIPROT:Q9C9V8; UNIPARC:UPI00000A8C1A; GB:AE005173; NID:g6553903; PII
C:Genetics:
A:Gene: T23K23.23
A:Map position: 1
Query Match 11.4%; Score 47; DB 2; Length 67;
Best Local Similarity 34.8%; Pred. No. 2.9e+02;
Matches 16; Conservative 5; Mismatches 13; Indels 12; Gaps 2;
QY 11 KEP--VRTLGLRAEIAEVAVEIGRPRDQVYMLKRWRFQQQAPGLG 54
||||| : : : ||| : : : |||
24 KEPEKIQPSLQQPEMRVLSEIKR-----RQRSRSPGLIG 59
Db

```

[illegible]

RESULT 12
JH0129
repressor protein cac - Escherichia coli plasmid RSF1010
N:Alternate names: repressor protein P
C:Species: Escherichia coli
A:Note: plasmid RSF1010 is a broad-host-range plasmid belonging to incompatibility group
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: JH0129; PS0292
R:Scholz, P.; Haring, V.; Wittmann-Liebold, B.; Ashman, K.; Bagdasarian, M.; Scherzinger,
Gene 75, 271-288, 1989
A:Title: Complete nucleotide sequence and gene organization of the broad-host-range plasm
A:Reference number: JH0123; MWID:89232758; PMID:2653965

RESULT 14
A75099
hypothetical protein PAB3293 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: A75099
R:Anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A:Reference number: A75001
A:Accession: A75099
A>Status: preliminary

Search completed: March 20, 2006, 08:05:27
Job time : 25 secs

A;Status: preliminary

OS *Pseudomonas putida*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ohmori D.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB054812; BAB62001.1; -; Genomic_DNA.
DR HSSP; Q9EZJ8; 1KU3.
DR GO; GO:0003899; F:DNA-directed RNA polymerase activity; IRA.

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OSJ162;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=TK0923;
OS Pyrococcus kodakaraensis (Thermococcus kodakaraensis).
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
OC NCBI_TaxId=69014;
OX [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=KOD1;
RC PubMed=15710748; DOI=10.1101/gr.3003105;
RA Fukui T., Acomi H., Kanai T., Matsumi R., Fujiwara S., Imanaka T.;
RT "Complete genome sequence of the hyperthermophilic archaeon
RT Thermococcus kodakaraensis KOD1 and comparison with Pyrococcus
RT genomes."
RL Genome Res. 15:352-363 (2005).
DR EMBL; AP006878; BAD85112.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 72 AA; 8420 MW; 605AF03D9F66F69F CRC64;

Query Match 13.7%; Score 56.5; DB 2; Length 72;
Best Local Similarity 34.7%; Pred. No. 3e+02;
Matches 17; Conservative 11; Mismatches 12; Indels 9; Gaps

Qy 1 VMDAVPARWK-EFV---RTGLREAEIEAVEVEIGRFRDQOYMLKR 44
Db 23 VKRAIEARIEFIEDIARRIGIDKEIEAIE---KARDEAWQEFKK 67

RESULT 5
Q7P321_FUSNV
ID Q7P321_FUSNV PRELIMINARY; PRT; 59 AA.
AC Q7P321;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Virulence-associated protein I.
GN Name=PNV0340;
OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OC NCBI_TaxId=209882;
OX [1]
RP NUCLEOTIDE SEQUENCE.
RC SFRAIN=ATCC 49256;
RA Karpatal V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,
RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
RA Haelkorn R., Overbeek R., Kyrpides N.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABF01000154; EAA23321.1; -; Genomic DNA.
DR Q7P321;
SQ SEQUENCE 59 AA; 6808 MW; 61C5DF19B318E86 CRC64;

Query Match 13.2%; Score 54.5; DB 2; Length 59;
Best Local Similarity 37.2%; Pred. No. 4e+02;
Matches 16; Conservative 5; Mismatches 21; Indels 1; Gaps

Qy 11 KEFVRTGLREAEIEA-VEVEIGRFRDQOYMLKRWQOQPAG 52
Db 9 KGMVQLGLPEKLETALINAEISISHDMIYRIVKTMHQKNYG 51

RESULT 6
Q9ZX19_9CAUD
ID Q9ZX19_9CAUD PRELIMINARY; PRT; 69 AA.
AC Q9ZX19;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Pseudomonas aeruginosa phage phi CTX, complete genome sequence.
OS Bacteriophage phi CTX.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC P2-like viruses.
OX NCBI_TaxID=35343;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=phiCTX-c;
RX MEDLINE=90014160; PubMed=2507866;
RA Hayaishi T., Kamio Y., Hishinuma P., Usami Y., Titani K., Terawaki Y.;
RT "Pseudomonas aeruginosa cytotoxin: the nucleotide sequence of the gene
RT and the mechanism of activation of the protoxin.";
RL Mol. Microbiol. 3:861-868(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=phiCTX-c;
RX MEDLINE=99157549; PubMed=10027959;
RA Nakayama K., Kanaya S., Ohnishi M., Terawaki Y., Hayashi T.;
RT "The complete nucleotide sequence of phiCTX, a cytotoxin-converting
RT phage of Pseudomonas aeruginosa: implications for phage evolution and
RT horizontal gene transfer via bacteriophage.";
RL Mol. Microbiol. 31:399-419(1999).
DR ENBL; AB008550; BAA36234.1; -; Genomic_DNA.
DR InterPro; IPR008861; Tail X.
DR PFAM; PF05489; Phage tail X; 1.
SQ SEQUENCE 69 AA; 7436 MW; D2E35A698F195CC0 CRC64;

Query Match 13.1%; Score 54; DB 2; Length 69;
Best Local Similarity 45.8%; Pred. No. 5.3e+02;
Matches 11; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 3 DAVPARRWKEFVRTGLREAEIA 26
DB 10 DTVEALCWRYHGTAGTVEAVLEA 33

RESULT 7
Q4ZBG0_9VIRU
ID Q4ZBG0_9VIRU PRELIMINARY; PRT; 78 AA.
AC Q4ZBG0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE ORF067.
OS Bacteriophage 71.
OC Viruses.
OX NCBI_TaxID=320844;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PubMed=15788529; DOI=10.1073/pnas.0501140102;
RA Kwan T., Liu J., Dubow M., Gros P., Pelletier J.;
RT "The complete genomes and proteomes of 27 Staphylococcus aureus
RT bacteriophages.";
RL Proc. Natl. Acad. Sci. U.S.A. 102:5174-5179(2005).
DR ENBL; AY954962; AAX91625.1; -; Genomic DNA.
SQ SEQUENCE 78 AA; 8987 MW; 1383AFA7A3A06887 CRC64;

Query Match 13.1%; Score 54; DB 2; Length 78;
Best Local Similarity 31.2%; Pred. No. 6e+02;
Matches 20; Conservative 10; Mismatches 28; Indels 6; Gaps 3;

QY 17 LGREAEIAVEVEIGFRDQYQYEMLK-RWRQQPAGLGAAYAAALRMGLDG----CVD 71
DB 12 MALKEHNKIKLSEIGVNRDTLSNMHIGRTKPSYVP-INGIYFALELTQEGRDIFNED 70

QY 72 LRSR 75
DB 71 LRKK 74

RESULT 8
Q6CZU0_ERWCT

06CZU0_ERWCT PRELIMINARY; PRT; 78 AA.
AC Q6CZU0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=ECA4061;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holvea M.C., Thomson N.R., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Atkin R., Bason N., Hauser H., Jagsels K., Moule S., Norbertczak H.,
RA Fraser A., Hance Z., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Ormond D., Price C., Birch P.R.J., Parkhill J., Toth I.K.;
RA Salmond G.P.C., Birn P.R.J., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
DR ENBL; BX950851; CAG76958.1; -; Genomic DNA.
DR InterPro; IPR008227; UCP006169.
DR InterPro; IPR010648; UPF0270.
DR PFAM; PF06794; UPF0270; 1.
DR PIRSF; PIRSF006169; UCP006169; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 78 AA; 8894 MW; CC29D8DC6F12B9C CRC64;

Query Match 13.1%; Score 54; DB 2; Length 78;
Best Local Similarity 36.0%; Pred. No. 6e+02;
Matches 18; Conservative 4; Mismatches 16; Indels 12; Gaps 2;

QY 41 MLKRWRRQQQAPGL-----GAVYAALERMGLDGCVDLRSRLQRG 79
DB 1 MIIPWQLDPTLDSIIESFVLREGTDYGEQER-SLAQKVEDIRSLSQSG 49

RESULT 9
Q8TYA5_METKA
ID Q8TYA5_METKA PRELIMINARY; PRT; 79 AA.
AC Q8TYA5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Predicted RNA-binding protein containing the S4 domain.
GN OrderedLocusNames=MK0398;
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014; DOI=10.1073/pnas.032671499;
RA Slesarev A.I., Mezhvaya K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natile D.A., Rogosin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozyavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
DR ENBL; AB010336; AAM01613.1; -; Genomic DNA.
DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro; IPR002942; S4.
DR PFAM; PF01479; S4; 1.
DR SMART; SM00363; S4; 1.

lank H.-B., Kramer W., Merkl R., Gottschalk G., Fritz H.-U.; RA Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarren J., RA Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.; RT "The genome of a motile marine *Synechococcus*"; RL Nature 424:1037-1042(2003).
RT Nature 424:1037-1042(2003).
at. Biotechnol. 22:547-553(2004).

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Job time : 108 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 20, 2006, 08:02:39 ; Search time 79 Seconds
(without alignments)

444.941 Million cell updates/sec

Title: US-10-081-280-6_COPY_338_417

Perfect score: 413

Sequence: 1 VMDVAPARRWKEFVRLTGLR.....ERMGLDGVEDLRSLRQRP 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 1293556

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: A_Geneseq_21.*

2: Geneseqp1980s.*

3: Geneseqp1990s.*

4: Geneseqp2000s.*

5: Geneseqp2001s.*

6: Geneseqp2002s.*

7: Geneseqp2003s.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	381	92.3	74	5	ABG31492 Human Apo
2	381	92.3	74	7	ADG98744 Apo-3/DR3
3	381	92.3	74	8	ADO40453 Human Apo
4	338	81.8	65	2	AAW93610 Human DR3
5	338	81.8	65	3	AAW93610 Human DR3
6	155	37.5	78	5	ABG31493 Human Apo
7	155	37.5	78	6	ADA49709 Death dom
8	155	37.5	78	7	ADG98745 TNFR1 dea
9	155	37.5	78	8	ADO40454 Human TNF
10	142	34.4	69	2	AAW93612 Human TNF
11	139	33.7	30	4	AAO08695 Human pol
12	136.5	33.1	68	3	AAW93612 Human TNF
13	118	28.6	64	2	AAW00208 Human TNF
14	105	25.4	75	7	ADG42594 NOV1 doma
15	94	22.8	76	8	ADO40451 Human Apo
16	83	20.1	67	3	AAW93613 Human DR5
17	82	19.9	67	2	AAW93613 Human CAR
18	77.5	18.8	67	3	AAW93613 Human CAR
19	74	17.9	45	4	AAW93613 Human CAR
20	74	17.9	45	4	AAW93613 Human CAR
21	74	17.9	45	4	AAW93613 Human CAR
22	70.5	17.1	77	6	ADA49713 Death dom
23	68	16.5	67	3	AAW93613 Human CAR
24	67	16.2	51	2	AAW93613 Human CAR

25	64.5	15.6	65	5	AAE24868	Chlamydia
26	64.5	15.6	65	5	AAE38911	Chlamydia
27	60	14.5	77	2	AAW62177	Nerve gro
28	60	14.5	77	8	ADJ25858	Nerve gro
29	60	14.5	77	9	ADZ48605	Nerve gro
30	57.5	13.9	63	2	AAW00206	Human Fas
31	57.5	13.9	68	2	AAW93611	Human Fas
32	57.5	13.9	68	3	AAW93611	Human Fas
33	57.5	13.9	68	4	AAW93611	Human Fas
34	57.5	13.9	77	6	AAW93611	Human Fas
35	57.5	13.9	77	7	AAW93611	Human Fas
36	57.5	13.9	77	8	AAW93611	Human Fas
37	57.5	13.9	77	9	AAW93611	Human Fas
38	57	13.8	65	5	AAE24866	Chlamydia
39	57	13.8	65	5	AAE38909	Chlamydia
40	57	13.8	71	5	AAE24857	Mouse NGF
41	57	13.8	71	5	AAE38900	Mouse NGF
42	56.5	13.7	73	8	ADN46273	Thermococ
43	56	13.6	65	5	AAE24856	Chlamydia
44	56	13.6	65	5	AAE38899	Chlamydia
45	55	13.3	60	4	AAU63529	Propionib

ALIGNMENTS

RESULT 1

ABG31492

ID ABG31492 standard; protein; 74 AA.

XX AC ABG31492;

XX AC ABG31492;

DT 21-NOV-2002 (first entry)

XX Human Apo-2Dcr associated protein #2.

DE Human Apo-2Dcr associated protein #2.

XX Human; Apo-2Dcr; Apo-2 ligand; programmed cell death; apoptosis;

KW neurodegenerative disease; autoimmune; inflammatory.

XX Homo sapiens.

XX US2002102706-A1.

XX 01-AUG-2002.

XX 21-JUN-2001; 2001US-00887879.

XX 18-JUN-1997; 97US-0049911P.

XX 12-JUN-1998; 98US-00096500.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Chuntharapai A, Gurney A, Kim KJ;

XX Wood WI;

XX WPI; 2002-697823/75.

XX Novel isolated Apo-2Dcr polypeptide useful for modulating apoptosis in

XX mammalian cells.

XX Disclosure; Page 37; 58pp; English.

XX The present invention relates to the isolation of novel human

XX polypeptides, designated Apo-2Dcr, and the polynucleotide sequences

XX encoding them. Apo-2Dcr is capable of binding Apo-2 ligand and is useful

XX for modulating programmed cell death or apoptosis in mammalian cells. Apo

XX -2Dcr can be used to produce apo-2Dcr antibodies which are useful

XX therapeutically, and can cross-react with other receptors for Apo-2

XX ligand to block excessive apoptosis in neurodegenerative diseases, or to

XX block potentially autoimmune or inflammatory effects. Apo-2Dcr antibodies

XX are also useful in immunohistochemistry staining assays or diagnostic

XX assays for Apo-2Dcr, e.g. detecting its expression in specific cells,

XX tissues or serum, and for the affinity purification of Apo-2Dcr from

CC recombinant cell culture or natural sources. The present sequence
CC represents a protein of unknown function relating to the present
CC invention. Note: The present sequence is given in the Seq listing but is
CC not mentioned elsewhere in the specification
XX
SQ Sequence 74 AA;

Query Match 92.3%; Score 381; DB 5; Length 74;
Best Local Similarity 100.0%; Pred. No. 5.8e-41;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWKQQPAGLGAVYAAL 60
DB 1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWKQQPAGLGAVYAAL 60

QY 61 ERMGLDGCVEDLRS 74
DB 61 ERMGLDGCVEDLRS 74

RESULT 2
ADG98744
ID ADG98744 standard; protein; 74 AA.
AC ADG98744;
XX
DT 11-MAR-2004 (first entry)
DE Apo-3/DR3 death domain protein.
XX
KW Apo-2; apoptosis; diagnosis; tissue-specific typing; transgenic animal;
KW cancer; gene therapy.
XX
OS Unidentified.
XX
FN US2003148455-A1.
XX
PD 07-AUG-2003.
XX
PF 06-NOV-2002; 2002US-00288917.

XX 15-MAY-1997; 97US-0046615P.
PR 09-FEB-1998; 98US-0074119P.
PR 14-MAY-1998; 98US-00079029.
PR 02-NOV-2001; 2001US-00052798.
XX
PA (GETH) GENENTECH INC.
XX
PI Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
XX
DR WPI; 2003-897574/82.
XX
PT New Apo-2 polypeptide or its extracellular or death domain sequence,
PT useful for modulating apoptosis in mammalian cancer cells or for
PT generating transgenic or knockout animals.
XX
PS Disclosure; Fig 2B; 64pp; English.

XX The present invention provides novel Apo-2 protein and the nucleic acid
CC encoding the protein. The invention is useful in inducing apoptosis in
CC mammalian cancer cells. The invention is also useful in diagnostic
CC procedures for tissue-specific typing and in generating transgenic
CC animals that are useful in development and screening of reagents. The
CC invention is also useful in gene therapy. The present sequence is
CC Apo3/DR3 death domain protein.
XX
SQ Sequence 74 AA;

Query Match 92.3%; Score 381; DB 7; Length 74;
Best Local Similarity 100.0%; Pred. No. 5.8e-41;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWKQQPAGLGAVYAAL 60

DB 1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWKQQPAGLGAVYAAL 60
QY 61 ERMGLDGCVEDLRS 74
DB 61 ERMGLDGCVEDLRS 74

RESULT 3
ADO40453
ID ADO40453 standard; protein; 74 AA.

AC ADO40453;
XX
DT 15-JUL-2004 (first entry)

XX Human Apo-3/DR3 protein.
DE
XX Apo-2 protein; apoptosis; cancer; tissue typing; transgenic animal;
KW gene therapy; human; Apo-3/DR3.
XX
OS Homo sapiens.

XX US2004009552-A1.
FN
XX
PD 15-JAN-2004.
XX
PF 25-APR-2003; 2003US-00423448.

XX 15-MAY-1997; 97US-0046615P.
PR 09-FEB-1998; 98US-0074119P.
PR 14-MAY-1998; 98US-00079029.
PR 02-NOV-2001; 2001US-00052798.
PR 06-NOV-2002; 2002US-00288917.
XX
PA (GETH) GENENTECH INC.

XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
XX
XX WPI; 2004-090468/09.

XX New Apo-2 polypeptides and encoding nucleic acid molecules, useful for
PT diagnosing, preventing or treating cancer, and in tissue typing or in
PT generating antibodies or transgenic animals.

PS Example 1; Fig 2B; 53pp; English.

XX The present invention provides novel Apo-2 polypeptide and the encoding
CC polynucleotide capable of modulating apoptosis. The invention is useful
CC in diagnosing, treating and preventing cancer, tissue typing, in
CC generating antibodies and transgenic animals. The invention is also
CC useful in gene therapy. The present sequence is human Apo-3/DR3 protein.
CC This sequence is used in the exemplification of the invention

XX Sequence 74 AA;

Query Match 92.3%; Score 381; DB 8; Length 74;
Best Local Similarity 100.0%; Pred. No. 5.8e-41;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWKQQPAGLGAVYAAL 60
DB 1 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWKQQPAGLGAVYAAL 60
QY 61 ERMGLDGCVEDLRS 74
DB 61 ERMGLDGCVEDLRS 74

RESULT 4
AAW93610
ID AAW93610 standard; protein; 65 AA.
XX

AC AAW93610;
XX
DT 18-JUN-1999 (first entry)
XX
DE Human DR3 protein fragment.
XX
XX Killer protein; adriamycin inducible; human; chromosome 8p21; diagnosis;
KW p53-inducible; apoptosis-mediating activity; treatment; animal model;
KW neoplastic disease; DR3.
XX
OS Homo sapiens.
XX
FN WO9902653-A1.
XX
XX
PD 21-JAN-1999.
XX
XX 10-JUL-1998; 98WO-US014495.
XX
PR 11-JUL-1997; 97US-0052305P.
PR 04-AUG-1997; 97US-0054710P.
PR 30-SEP-1997; 97US-0060473P.
PR 11-MAR-1998; 98US-0077526P.
PR 11-MAR-1998; 98US-0077628P.
PR 11-MAR-1998; 98US-0077661P.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
XX
PI El-Deiry WS;
XX
XX
DR WPI; 1999-120857/10.
XX
XX
PT A new nucleic acid encodes a p53-induced protein (Killer) - which induces
PT apoptosis and is useful in the diagnosis and treatment of neoplastic
PT diseases.
XX
PS Disclosure; Page 46; 65pp; English.
XX
CC This invention describes a novel human adriamycin-inducible killer
CC protein located on chromosome 8p21, which also has p53-inducible,
CC apoptosis-mediating activity and comprises an amino-terminal
CC extracellular receptor, transmembrane and death domains. The nucleic acid
CC molecule which encodes the protein, it's encoded signal transduction
CC protein and antibodies of the invention are useful in the diagnosis and
CC treatment of neoplastic diseases. The invention is also useful for the
CC production of animal model systems
XX
SQ Sequence 65 AA;

Query Match 81.8%; Score 338; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.7e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RWKEFVTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWROOQAPGLGAVYAALERMGLDGC 68
DB 1 RWKEFVTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWROOQAPGLGAVYAALERMGLDGC 60

QY 69 VEDLR 73
DB 61 VEDLR 65

RESULT 5
AAB26990
ID AAB26990 standard; protein; 65 AA.
XX
AC AAB26990;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human DR3 death domain.
XX
XX Human; tumour necrosis factor; TNF; TR9 receptor; immunosuppressive;
KW antiinflammatory; cardiant; antiasthmatic; antidiabetic; antiallergic;
KW

KW antiathritic; antirheumatic; anti-HIV; anticonvulsant; cytostatic;
KW neuroprotective; gene therapy; Death Domain Containing Receptor 6;
KW common variable immunodeficiency; X-linked agammaglobulinaemia;
KW severe combined immunodeficiency; Wiskott-Aldrich syndrome;
KW autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;
KW multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;
KW cardiovascular disease; neurological disease; protein coordinate data;
KW osteoprotegerin; DR3.
XX
OS Homo sapiens.
XX
FN WO200056862-A1.
XX
XX
PD 28-SEP-2000.
XX
XX 16-MAR-2000; 2000WO-US006831.
XX
PR 24-MAR-1999; 99US-0126019P.
PR 14-MAY-1999; 99US-0134220P.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ni J, Gentz RL, Yu G, Fan P;
XX
XX WPI; 2000-594575/56.
XX
XX Nucleic acid molecule encoding a human tumor necrosis factor receptor,
PT known as TR9, useful for treating, preventing and diagnosing severe
PT combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy
PT and cancer.
XX
PS Disclosure; Fig 4C; 220pp; English.
XX
XX The present sequence is the death domain of DR3. It was used for
CC comparison to a domain of a novel human tumour necrosis factor receptor,
CC designated TR9. The TR9 receptor is also known as Death Domain Containing
CC Receptor 6. TR9 polypeptides, polynucleotides or agonists are useful for
CC treating, preventing or diagnosing common variable immunodeficiency, X-
CC linked agammaglobulinaemia, severe combined immunodeficiency and Wiskott-
CC Aldrich syndrome, autoimmune diseases (such as rheumatoid arthritis,
CC allergic encephalomyelitis, multiple sclerosis, diabetes mellitus and
CC asthma), HIV infection, epilepsy, cancer, cardiovascular diseases and
CC other neurological diseases
XX
SQ Sequence 65 AA;

Query Match 81.8%; Score 338; DB 3; Length 65;
Best Local Similarity 100.0%; Pred. No. 1.7e-35;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RWKEFVTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWROOQAPGLGAVYAALERMGLDGC 68
DB 1 RWKEFVTLGLREAEIEAVEVEIGRFRDQOQYEMLKRWROOQAPGLGAVYAALERMGLDGC 60

QY 69 VEDLR 73
DB 61 VEDLR 65

RESULT 6
ABG31493
ID ABG31493 standard; protein; 78 AA.
XX
AC ABG31493;
XX
DT 21-NOV-2002 (first entry)
XX
DE Human Apo-2bcr associated protein #3.
XX
XX Human; Apo-2bcr; Apo-2 ligand; programmed cell death; apoptosis;
KW neurodegenerative disease; autoimmune; inflammatory.
XX
OS Homo sapiens.

XX US2002102706-A1.
XX 01-AUG-2002.
XX 21-JUN-2001; 2001US-00887879.
XX 18-JUN-1997; 97US-0049911P.
XX 12-JUN-1998; 98US-00096500.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Chuntharapai A, Gurney A, Kim KJ;
XX Wood WI;
XX WPI; 2002-697823/75.
XX Novel isolated Apo-2Dcr polypeptide useful for modulating apoptosis in
XX mammalian cells.
XX Disclosure; Page 37; 58pp; English.
XX The present invention relates to the isolation of novel human
XX polypeptides, designated Apo-2Dcr, and the polynucleotide sequences
XX encoding them. Apo-2Dcr is capable of binding Apo-2 ligand and is useful
XX for modulating programmed cell death or apoptosis in mammalian cells. Apo
XX -2Dcr can be used to produce apo-2Dcr antibodies which are useful
XX therapeutically, and can cross-react with other receptors for Apo-2
XX ligand to block excessive apoptosis in neurodegenerative diseases, or to
XX block potentially autoimmune or inflammatory effects. Apo-2Dcr antibodies
XX are also useful in immunohistochemistry staining assays or diagnostic
XX assays for Apo-2Dcr, e.g. detecting its expression in specific cells,
XX tissues or serum, and for the affinity purification of Apo-2Dcr from
XX recombinant cell culture or natural sources. The present sequence
XX represents a protein of unknown function relating to the present
XX invention. Note: The present sequence is given in the Seq listing but is
XX not mentioned elsewhere in the specification
XX Sequence 78 AA;
XX Query Match 37.5%; Score 155; DB 5; Length 78;
XX Best Local Similarity 46.1%; Pred. No. 8e-12;
XX Matches 35; Conservative 13; Mismatches 24; Indels 4; Gaps 2;
QY 1 VMDAVPARRWKEFVRLTGLRBAEIEAVEVEIGR-FRDOQYEMLKRWQQQP---AGLGAV 56
Db 1 VVENVPPLRWKEFVRLGLSDHEIDRLQLONGRCLREAQYSMLATWRRTPRREATLELL 60
QY 57 YAALERMGIDGCVEDL 72
Db 61 GRVLRDMDLLGCLEDI 76
RESULT 7
ID ADA49709 standard; protein; 78 AA.
XX ADA49709;
XX 20-NOV-2003 (first entry)
XX Death domain of human TNFR1 (htnFR1) protein.
XX Apo-2 ligand inhibitor; Apo-2Li; Apo-3; apoptosis; affinity;
XX competitive-type receptor; binding assay; cancer cell; human;
XX TNF receptor family; htnFR1; death domain; cytostatic.
XX Homo sapiens.
XX US2002192729-A1.
XX 19-DEC-2002.
XX (GETH) GENENTECH INC.

PF 28-MAR-2002; 2002US-00112793.
XX 01-APR-1996; 96US-00625328.
XX 23-SEP-1996; 96US-00710802.
XX 31-MAR-1997; 97US-00828683.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ;
XX WPI; 2003-657226/62.
XX Novel isolated biologically active Apo-2 ligand inhibitor polypeptide, or
XX Apo-3 polypeptide which induces or stimulates apoptotic activity, useful
XX in diagnostic assays.
XX Disclosure; Fig 6; 53pp; English.
XX The present invention relates to the isolation of a biologically active
XX Apo-2 ligand inhibitor (Apo-2Li) or Apo-3, and the polynucleotide
XX sequences encoding them. Apo-2Li and Apo-3, are involved in apoptosis. The
XX Apo-2Li and Apo-3 polypeptides are useful in diagnostic assays. Apo-3 or
XX is useful for generating antibodies, as standards in assays for Apo-3 or
XX Apo-2Li, in affinity purification techniques, and in competitive-type
XX receptor binding assays when labelled with radioiodine, enzymes or
XX fluorophores. Agonistic Apo-3 antibodies are useful for stimulating or
XX inducing apoptosis in cancer cells, and thus have therapeutic utility.
XX The present sequence represents the death domain of a human TNF receptor
XX family protein. This sequence is compared with the death domain of human
XX Apo-3.
XX Sequence 78 AA;
XX Query Match 37.5%; Score 155; DB 6; Length 78;
XX Best Local Similarity 46.1%; Pred. No. 8e-12;
XX Matches 35; Conservative 13; Mismatches 24; Indels 4; Gaps 2;
QY 1 VMDAVPARRWKEFVRLTGLRBAEIEAVEVEIGR-FRDOQYEMLKRWQQQP---AGLGAV 56
Db 1 VVENVPPLRWKEFVRLGLSDHEIDRLQLONGRCLREAQYSMLATWRRTPRREATLELL 60
QY 57 YAALERMGIDGCVEDL 72
Db 61 GRVLRDMDLLGCLEDI 76
RESULT 8
ID ADG98745 standard; protein; 78 AA.
XX ADG98745;
XX 11-MAR-2004 (first entry)
XX TNFR1 death domain protein.
XX Apo-2; apoptosis; diagnosis; tissue-specific typing; transgenic animal;
XX cancer; gene therapy.
XX Unidentified.
XX US2003148455-A1.
XX 07-AUG-2003.
XX 06-NOV-2002; 2002US-00288917.
XX 15-MAY-1997; 97US-0046615P.
XX 09-FEB-1998; 98US-0074119P.
XX 14-MAY-1998; 98US-00079029.
XX 02-NOV-2001; 2001US-00052798.
XX (GETH) GENENTECH INC.

Query Match 34.4%; Score 142; DB 2; Length 69;
Best Local Similarity 47.1%; Pred. No. 3.3e-10;
Matches 32; Conservative 11; Mismatches 21; Indels 4; Gaps 2;

QY 9 RWKEFVTLGLREAEIEAVEVEIGR-FRDOQYEMLKRWROQP---AGLGVAAALERMG 64
DB 1 RWKEFVRLGLSDHEIDRLQNGRCLEAQAQYSLMATWRRTPREATLELLGRLVDM 60

QY 65 LDGCVEDL 72
DB 61 LGCLEDI 68

RESULT 11
AA08695
ID AA08695 standard; protein; 30 AA.
AC AA08695;
XX
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 22587.

Human; cytokine; cell proliferation; cell differentiation; gene therapy;
vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorders; arthritis; inflammation.

XX Homo sapiens.

OS WO200164835-A2.

PN 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US004927.

XX 28-FEB-2000; 2000US-00515126.

PR 18-MAY-2000; 2000US-00577409.

XX (HYSE-) HYSEQ INC.

PA Tang YT, Liu C, Drmanac RT;

XX WPI: 2001-514838/56.

DR N-PSDB; AAI88626.

XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
and treating e.g. leukemia, inflammation and immune disorders.

XX Claim 20; SEQ ID NO 22587; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to
cytokine, cell proliferation or cell differentiation or which may induce
production of other cytokines in other cell populations. The
polynucleotides and polypeptides are useful in gene therapy, vaccines or
peptide therapy. The polypeptides have various cytokine-like activities,
e.g. stem cell growth factor activity, haematopoiesis regulating
activity, tissue growth factor activity, immunomodulatory activity and
activin/inhibin activity and may be useful in the diagnosis and/or
treatment of cancer, leukaemia, nervous system disorders, arthritis and
inflammation. Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 30 AA;

Query Match 33.7%; Score 139; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 GAVYAALERMGLDGCVEDLRLQGP 80

DB 4 GAVYAALERMGLDGCVEDLRLQGP 30

RESULT 12

AA026989

ID AAB26989 standard; protein; 68 AA.

XX AAB26989;
AC

XX 02-FEB-2001 (first entry)

XX Human TNFR 1 death domain.
XX

Human; tumour necrosis factor; TNF; TR9 receptor; immunosuppressive;
anti-inflammatory; cardiant; antidiabetic; antiallergic;
antiathritic; antirheumatic; anti-HIV; anticonvulsant; cytostatic;
neuroprotective; gene therapy; Death Domain Containing Receptor 6;
common variable immunodeficiency; X-linked agammaglobulinaemia;
severe combined immunodeficiency; Wiskott-Aldrich syndrome;
autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;
multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;
cardiovascular disease; neurological disease; protein coordinate data;
osteoprotegerin; TNFR 1.

XX Homo sapiens.

OS WO200056862-A1.

PN 28-SEP-2000.

XX 16-MAR-2000; 2000WO-US006831.

XX 24-MAR-1999; 99US-0126019P.

PR 14-MAY-1999; 99US-0134220P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ni J, Gentz RL, Yu G, Fan P;

XX WPI: 2000-594575/56.

XX Nucleic acid molecule encoding a human tumor necrosis factor receptor,
known as TR9, useful for treating, preventing and diagnosing severe
combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy
and cancer.

XX Disclosure; Fig 4C; 220pp; English.

XX The present sequence is the death domain of TNFR 1. It was used for
comparison to a domain of a novel human tumour necrosis factor receptor,
designated TR9. The TR9 receptor is also known as Death Domain Containing
Receptor 6. TR9 polypeptides, polynucleotides or agonists are useful for
treating, preventing or diagnosing common variable immunodeficiency, X-
linked agammaglobulinaemia, severe combined immunodeficiency and Wiskott-
Aldrich syndrome, autoimmune diseases (such as rheumatoid arthritis,
allergic encephalomyelitis, multiple sclerosis, diabetes mellitus and
asthma), HIV infection, epilepsy, cancer, cardiovascular diseases and
other neurological diseases

XX Sequence 68 AA;

Query Match 33.1%; Score 136.5; DB 3; Length 68;
Best Local Similarity 46.3%; Pred. No. 1.6e-09;
Matches 31; Conservative 12; Mismatches 21; Indels 3; Gaps 2;

QY 9 RWKEFVTLGLREAEIEAVEVEIGR-FRDOQYEMLKRWRO---QOPAGLGVAAALERMGL 65
DB 1 RWKEFVRLGLSDHEIDRLQNGRCLEAQAQYSLMATWRRTPREATLELLGRLVDM 60

QY 66 DGCVEDL 72
DB 61 LGCLEDI 67

```
RESULT 13
AAW00208
ID AAW00208 standard; peptide; 64 AA.
XX
XX AC AAW00208;
XX
XX DT 16-APR-1997 (first entry)
XX
XX DE Human p55 tumour necrosis factor receptor death domain motif.
XX
XX KW Death domain; regulatory protein; NGF-R; nerve growth receptor; FAS-R;
XX KW Fas ligand receptor; Fas/ABO1; ankyrin 1; p55 TNF-R;
XX KW tumour necrosis factor receptor; MORT1; cell cytotoxicity; HIV;
XX KW human immunodeficiency virus; cancer; neoplasia; disease.
XX
XX OS Homo sapiens.
XX
XX PN WO9625941-A1.
XX
XX PD 29-AUG-1996.
XX
XX PF 15-FEB-1996; 96WO-US002326.
XX
XX PR 22-FEB-1995; 95IL-00112742.
XX
XX PR 13-SEP-1995; 95IL-00115289.
XX
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX PA (WEIN/) WEINURZEL H.
XX
XX FI Wallach D, Boldin MP, Varfolomeev EE, Pancer Z, Mett I;
XX FI Goncharov TM;
XX
XX DR WPI; 1996-402125/40.
XX
XX PT Modulator of regulatory cellular events mediated by "death domain" contg.
XX PT regulatory proteins - useful for modulating functions mediated in cells
XX PT by proteins contg the death domain.
XX
XX PS Claim 9; Fig 1; 74pp; English.
XX
XX CC AAW00207 shows the death domain of the p55 tumour necrosis factor
XX CC receptor (p55 TNF-R). The death domain (DD) of human Fas-ligand receptor
XX CC (FAS-R), ankyrin 1, nerve growth factor receptor (NGF-R) and MORT-1
XX CC (which binds to the intracellular portion of (FAS-R)) are also given (see
XX CC AAW00206-07 and AAW00209-W00210). These DDs are used to identify
XX CC compounds capable of modulating activity of the regulatory proteins (p55,
XX CC NGF, TNF and FAS-R ligand, MORT-1) via interaction with the DDs. Such
XX CC modulators which may be antibodies, antisense sequences or ribozymes
XX CC (which can affect the cellular mRNA sequences encoding the proteins) and
XX CC are useful for modulation of effects of the regulatory proteins within
XX CC the cell. Tumour cells, HIV-infected cells or other diseased cells can be
XX CC treated by targeting the cells with animal viral vectors encoding the
XX CC modulators and a viral surface antigen capable of binding to a specific
XX CC receptor. The DDs are characterised by having groups of common amino acid
XX CC residues Trp, Ala, Asp, Glu, Thr, Arg and Tyr within locations that can
XX CC be aligned to show homology
XX
XX SQ Sequence 64 AA;
Query Match 28.6%; Score 118; DB 2; Length 64;
Best Local Similarity 42.6%; Pred. No. 3.7e-07;
Matches 29; Conservative 10; Mismatches 17; Indels 12; Gaps 3;

QY 10 WKFEVFTLGLREAEIEAVEVEIGR-FRDOQYEMLRKRWQOQAGLGVAVYALRMG----- 64
DB 1 WKFEVRLGLSDHEDIDLELQNGRCLREAQYSMLATWRRTRPR-----EATLELLGRVLR 56
QY 65 ---LDGCV 69
DB 57 DHDLGLGL 64
```

```
RESULT 14
ADG42594
ID ADG42594 standard; protein; 75 AA.
XX
XX AC ADG42594;
XX
XX DT 26-FEB-2004 (first entry)
XX
XX DE NOVI domain analysis associated protein seq id 47.
XX
XX KW cytostatic; gene therapy; NOVX-agonist; NOVX-antagonist; pharmaceutical;
XX KW NOVX-associated disorder; cancer; NOVX; domain analysis.
XX
XX OS Unidentified.
XX
XX PN US2003204052-A1.
XX
XX PD 30-OCT-2003.
XX
XX PF 04-OCT-2001; 2001US-00970944.
XX
XX PR 04-OCT-2000; 2000US-0237862P.
XX
XX PA (HERR/) HERRMANN J L.
XX PA (RAST/) RASTELLI L.
XX PA (SHIM/) SHIMKETS R A.
XX
XX PI Herrmann JL, Rastelli L, Shimkets RA;
XX PI WPI; 2003-900673/82.
XX
XX PT New NOVX gene or NOVX-specific antibody, useful for preparing a
XX PT composition for treating or preventing a NOVX-associated disorder, e.g.,
XX PT cancer.
XX
XX PS Disclosure; SEQ ID NO 47; 118pp; English.
XX
XX CC The invention describes a new isolated polypeptide comprising: a
XX CC polypeptide or its mature form comprising a sequence not given in the
XX CC specification; or a variant of (A), where one or more amino acid residues
XX CC in the variant differs in no more than 15% from the amino acid sequence
XX CC of the mature form. The pharmaceutical composition may be administered
XX CC via oral, transdermal, rectal or parenteral route. The polypeptide,
XX CC nucleic acid or antibody is useful for preparing a composition for
XX CC treating or preventing a NOVX-associated disorder, e.g., cancer. This is
XX CC the amino acid sequence of a protein associated with analysis of domains
XX CC in human NOVI protein.
XX
XX SQ Sequence 75 AA;
Query Match 25.4%; Score 105; DB 7; Length 75;
Best Local Similarity 35.3%; Pred. No. 2.1e-05;
Matches 24; Conservative 12; Mismatches 30; Indels 2; Gaps 1;

QY 1 VMDAVPARRWKBFVFTLGLREAEIEAVEVEIGRFRDOQYEMLRKRWQO--QPAGLGAVYA 58
DB 6 LLDDPLGRWRRLARKLGLSEEDIQIENHENPLASPTYQLLDIWEQRGKGNATVGTLL 65
QY 59 ALRMRGLD 66
DB 66 ALRMRGRD 73

RESULT 15
ADO40451
ID ADO40451 standard; protein; 76 AA.
XX
XX AC ADO40451;
XX
XX DT 15-JUL-2004 (first entry)
XX
XX DE Human Apo-2 protein #2.
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XX Apo-2 protein; apoptosis; cancer; tissue typing; transgenic animal;
KW gene therapy; human.
XX Homo sapiens.
OS
XX US2004009552-A1.
FN
XX 15-JAN-2004.
PD
XX 25-APR-2003; 2003US-00423448.
PF
XX 15-MAY-1997; 97US-0046615P.
PR 09-FEB-1998; 98US-0074119P.
PR 14-MAY-1998; 98US-00079029.
PR 02-NOV-2001; 2001US-00052798.
PR 06-NOV-2002; 2002US-00288917.
XX
XX (GETH) GENENTECH INC.
PA
XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim KJ;
PI
XX WPI; 2004-090468/09.
DR
XX New Apo-2 polypeptides and encoding nucleic acid molecules, useful for
XX diagnosing, preventing or treating cancer, and in tissue typing or in
PT generating antibodies or transgenic animals.
PT
XX Example 1; SEQ ID NO 14; 53pp; English.
PS
XX The present invention provides novel Apo-2 polypeptide and the encoding
CC polynucleotide capable of modulating apoptosis. The invention is useful
CC in diagnosing, treating and preventing cancer, tissue typing, in
CC generating antibodies and transgenic animals. The invention is also
CC useful in gene therapy. The present sequence is human Apo-2 protein. This
CC sequence is used in the exemplification of the invention
XX
XX Sequence 76 AA;
SQ
Query Match 22.8%; Score 94; DB 8; Length 76;
Best Local Similarity 34.4%; Pred. No. 0.00056;
Matches 22; Conservative 11; Mismatches 29; Indels 2; Gaps 1;
QY 3 DAVPARRWKEFVRTGLREAEIEAVEVEIGRFRDQOQYEMLKRW--RQOQPAGLGAVYAAL 60
Db 3 DLVPFDSNEPLMKRLGLMDNEIKVAKAEAGHRDLYTMTLIKWNKNGRDSVHTLLDAL 62
QY 61 ERMG 64
Db 63 ETIG 66
Search completed: March 20, 2006, 08:04:07
Job time : 81 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 20, 2006, 08:04:14 ; Search time 44 Seconds
(without alignments)
759.690 Million cell updates/sec

Title: US-10-081-280-6_COPY_338_417

Perfect score: 413

Sequence: 1 VMDVAPARWKEFVTLGLR.....ERMGLDGCVEDLRSRLQRP 80

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 736366

Minimum DB seq length: 0

Maximum DB seq length: 80

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	381	92.3	74	3	US-09-887-879-15
2	381	92.3	74	3	US-09-992-964-15
3	381	92.3	74	4	US-10-207-295-9
4	381	92.3	74	4	US-10-242-383-15
5	338	81.8	65	3	US-09-756-854-24
6	338	81.8	65	4	US-10-041-574-24
7	338	81.8	65	4	US-10-834-966-24
8	338	81.8	65	6	US-11-148-333-24
9	155	37.5	78	3	US-09-887-879-16
10	155	37.5	78	3	US-09-992-964-16
11	155	37.5	78	4	US-10-112-793-23
12	155	37.5	78	4	US-10-207-295-10
13	155	37.5	78	4	US-10-242-383-16
14	136.5	33.1	68	3	US-09-756-854-23
15	136.5	33.1	68	4	US-10-041-574-23
16	136.5	33.1	68	6	US-10-834-966-23
17	136.5	33.1	68	6	US-11-148-333-23
18	118	28.6	64	4	US-10-035-408-3
19	94	22.8	76	4	US-10-207-295-7
20	83	20.1	67	3	US-09-756-854-26
21	83	20.1	67	4	US-10-041-574-26
22	83	20.1	67	4	US-10-834-966-26
23	83	20.1	67	6	US-11-148-333-26
24	77.5	18.8	67	6	US-10-791-513-5
25	74	17.9	76	4	US-10-207-295-8
26	70.5	17.1	77	4	US-10-112-793-27
27	70.5	17.1	77	4	US-10-287-594-7

28	68	16.5	67	3	US-09-756-854-25	Sequence 25, Appl
29	68	16.5	67	4	US-10-041-574-25	Sequence 25, Appl
30	68	16.5	67	4	US-10-834-966-25	Sequence 25, Appl
31	68	16.5	67	6	US-11-148-333-25	Sequence 25, Appl
32	64.5	15.6	65	4	US-10-001-254-56	Sequence 56, Appl
33	64.5	15.6	65	6	US-11-090-425-56	Sequence 56, Appl
34	63	15.3	62	4	US-10-424-599-188281	Sequence 188281,
35	60	14.5	77	5	US-10-656-250-118	Sequence 118, App
36	57.5	13.9	63	4	US-10-035-408-1	Sequence 1, Appli
37	57.5	13.9	68	3	US-09-756-854-22	Sequence 22, Appl
38	57.5	13.9	68	3	US-09-796-692-721	Sequence 721, App
39	57.5	13.9	68	4	US-10-041-574-22	Sequence 22, Appl
40	57.5	13.9	68	4	US-10-040-862-721	Sequence 721, App
41	57.5	13.9	68	4	US-10-057-475B-721	Sequence 721, App
42	57.5	13.9	68	4	US-10-154-884B-721	Sequence 721, App
43	57.5	13.9	68	4	US-10-764-324-721	Sequence 721, App
44	57.5	13.9	68	4	US-10-834-966-22	Sequence 22, Appl
45	57.5	13.9	68	6	US-11-148-333-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1

US-09-887-879-15
; Sequence 15, Application US/09887879
; Patent No. US20020102706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chuntharapal, Anan
; APPLICANT: Gurney, Austin
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Apo-2DCR
; FILE REFERENCE: F1110P1
; CURRENT APPLICATION NUMBER: US/09/887,879
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/096,500
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/049,911
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 15
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-887-879-15

Query Match 92.3%; Score 381; DB 3; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.3e-38;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VMDVAPARWKEFVTLGLRREAEIEAVEVEIGRFRDQOYEMLRWQOQOQAGLVYAAAL 60
Db 1 VMDVAPARWKEFVTLGLRREAEIEAVEVEIGRFRDQOYEMLRWQOQOQAGLVYAAAL 60
QY 61 ERMGLDGCVEDLRS 74
Db 61 ERMGLDGCVEDLRS 74

RESULT 2

US-09-992-964-15
; Sequence 15, Application US/09992964
; Patent No. US20020161202A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin
; APPLICANT: Gurney, Austin
; APPLICANT: Wood, William
; TITLE OF INVENTION: Apo-2DCR
; FILE REFERENCE: P1110

Mon Mar 20 08:26:42 2006

us-10-081-280-6_copy_338_417.rapbm

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; FILE REFERENCE: P1110P1
; CURRENT APPLICATION NUMBER: US/09/992,964
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 08/878,168
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 15
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-964-15

Query Match          92.3%; Score 381; DB 3; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.3e-38;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAAL 60
Db 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAAL 60

QY 61 ERMGLDGCVEDLRS 74
Db 61 ERMGLDGCVEDLRS 74

RESULT 3
US-10-207-295-9
; Sequence 9, Application US/10207295
; Publication No. US20030017161A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung Jin
; TITLE OF INVENTION: APO-2 RECEPTOR
; FILE REFERENCE: 11669.28US04
; CURRENT APPLICATION NUMBER: US/10/207,295
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/09/020,746
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 08/857,216
; PRIOR FILING DATE: 1997-05-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-295-9

Query Match          92.3%; Score 381; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.3e-38;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAAL 60
Db 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAAL 60

QY 61 ERMGLDGCVEDLRS 74
Db 61 ERMGLDGCVEDLRS 74

RESULT 4
US-10-242-383-15
; Sequence 15, Application US/10242383
; Publication No. US20030138915A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Gurney, Austin
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: APO-2DCR

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; FILE REFERENCE: P1110P1
; CURRENT APPLICATION NUMBER: US/10/242,383
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US/09/887,879
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/096,500
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/049,911
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 15
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-242-383-15

Query Match          92.3%; Score 381; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.3e-38;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAAL 60
Db 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGRFRDQOQYEMLKRWROQOPAGLGAVYAAL 60

QY 61 ERMGLDGCVEDLRS 74
Db 61 ERMGLDGCVEDLRS 74

RESULT 5
US-09-756-854-24
; Sequence 24, Application US/09756854
; Patent No. US20020164684A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,854
; FILING DATE: 10-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,094
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoover, Kenley K.
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF375
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 65 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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; SEQUENCE DESCRIPTION: SEQ ID NO: 24;
US-09-756-854-24

Query Match      81.8%; Score 338; DB 3; Length 65;
Best Local Similarity 100.0%; Pred. No. 2e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RWKEFVRTGLGREAIEAVEVEIGRFRDQYEMLKRWRRQQQPAGLGAVYAALERMGLDGC 68
DB 1 RWKEFVRTGLGREAIEAVEVEIGRFRDQYEMLKRWRRQQQPAGLGAVYAALERMGLDGC 60

QY 69 VEDLR 73
DB 61 VEDLR 65

RESULT 6
US-10-041-574-24
; Sequence 24, Application US/10041574
; Publication No. US20020168359A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/10/041,574
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/527,236
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-041-574-24

Query Match      81.8%; Score 338; DB 4; Length 65;
Best Local Similarity 100.0%; Pred. No. 2e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RWKEFVRTGLGREAIEAVEVEIGRFRDQYEMLKRWRRQQQPAGLGAVYAALERMGLDGC 68
DB 1 RWKEFVRTGLGREAIEAVEVEIGRFRDQYEMLKRWRRQQQPAGLGAVYAALERMGLDGC 60

QY 69 VEDLR 73
DB 61 VEDLR 65

RESULT 8
US-11-148-333-24
; Sequence 24, Application US/11148333
; Publication No. US20050239123A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375D1
; CURRENT APPLICATION NUMBER: US/11/148,333
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 65
; TYPE: PRT
; ORGANISM: human
US-11-148-333-24

Query Match      81.8%; Score 338; DB 6; Length 65;
Best Local Similarity 100.0%; Pred. No. 2e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RWKEFVRTGLGREAIEAVEVEIGRFRDQYEMLKRWRRQQQPAGLGAVYAALERMGLDGC 68
DB 1 RWKEFVRTGLGREAIEAVEVEIGRFRDQYEMLKRWRRQQQPAGLGAVYAALERMGLDGC 60

QY 69 VEDLR 73
DB 61 VEDLR 65

RESULT 9
US-09-887-879-16
; Sequence 24, Application US/10834966
; Publication No. US20040197870A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/10/834,966
; CURRENT FILING DATE: 2004-04-30
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; PRIOR APPLICATION NUMBER: US/10/041,574
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/527,236
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-834-966-24

Query Match      81.8%; Score 338; DB 4; Length 65;
Best Local Similarity 100.0%; Pred. No. 2e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RWKEFVRTGLGREAIEAVEVEIGRFRDQYEMLKRWRRQQQPAGLGAVYAALERMGLDGC 68
DB 1 RWKEFVRTGLGREAIEAVEVEIGRFRDQYEMLKRWRRQQQPAGLGAVYAALERMGLDGC 60

QY 69 VEDLR 73
DB 61 VEDLR 65

RESULT 8
US-11-148-333-24
; Sequence 24, Application US/11148333
; Publication No. US20050239123A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375D1
; CURRENT APPLICATION NUMBER: US/11/148,333
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 65
; TYPE: PRT
; ORGANISM: human
US-11-148-333-24

Query Match      81.8%; Score 338; DB 6; Length 65;
Best Local Similarity 100.0%; Pred. No. 2e-33;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RWKEFVRTGLGREAIEAVEVEIGRFRDQYEMLKRWRRQQQPAGLGAVYAALERMGLDGC 68
DB 1 RWKEFVRTGLGREAIEAVEVEIGRFRDQYEMLKRWRRQQQPAGLGAVYAALERMGLDGC 60

QY 69 VEDLR 73
DB 61 VEDLR 65

RESULT 9
US-09-887-879-16
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US-10-112-793-23
; Sequence 23, Application US/10112793
; Publication No. US20020192729A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/112,793
; FILING DATE: 28-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,683A
; FILING DATE: 31-Mar-1997
; APPLICATION NUMBER: 08/625328
; FILING DATE: 1-Apr-1996
; APPLICATION NUMBER: 08/710802
; FILING DATE: 23-Sep-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1007P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 78 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
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Query Match 37.5%; Score 155; DB 4; Length 78;
Best Local Similarity 46.1%; Pred. No. 5.4e-11;
Matches 35; Conservative 13; Mismatches 24; Indels 4; Gaps 2;
QY 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGR-FRDOQYEMLKRWQOQP---AGLGAV 56
DB 1 VVENVPPLRWKEFVRRGLSDHEIDRLQNGRCLEAQYSMLATWRRTPRREATLELL 60
QY 57 YAALERMGLDGCVEDL 72
DB 61 GRVLDMDLGLGLEDI 76
RESULT 12
US-10-295-10
; Sequence 10, Application US/10207295
; Publication No. US20030017161A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Kim, Kyung Jin
; TITLE OF INVENTION: Apo-2 RECEPTOR
; FILE REFERENCE: 11669.28US04
; CURRENT APPLICATION NUMBER: US/10/207,295
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US/09/020,746
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 08/857,216

US-09-887-879-16
; Sequence 16, Application US/09887879
; Patent No. US20020102706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Gurney, Austin
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Apo-2Dcr
; FILE REFERENCE: P110P1
; CURRENT APPLICATION NUMBER: US/09/887,879
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/096,500
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/049,911
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 16
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-887-879-16
Query Match 37.5%; Score 155; DB 3; Length 78;
Best Local Similarity 46.1%; Pred. No. 5.4e-11;
Matches 35; Conservative 13; Mismatches 24; Indels 4; Gaps 2;
QY 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGR-FRDOQYEMLKRWQOQP---AGLGAV 56
DB 1 VVENVPPLRWKEFVRRGLSDHEIDRLQNGRCLEAQYSMLATWRRTPRREATLELL 60
QY 57 YAALERMGLDGCVEDL 72
DB 61 GRVLDMDLGLGLEDI 76
RESULT 10
US-09-992-964-16
; Sequence 16, Application US/09992964
; Patent No. US20020161202A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin
; APPLICANT: Gurney, Austin
; APPLICANT: Wood, William
; TITLE OF INVENTION: Apo-2Dcr
; FILE REFERENCE: P110
; CURRENT APPLICATION NUMBER: US/09/992,964
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 08/878,168
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 16
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-964-16
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Best Local Similarity 46.1%; Pred. No. 5.4e-11;
Matches 35; Conservative 13; Mismatches 24; Indels 4; Gaps 2;
QY 1 VMDAVPARRWKEFVRTGLREAEIEAVEVEIGR-FRDOQYEMLKRWQOQP---AGLGAV 56
DB 1 VVENVPPLRWKEFVRRGLSDHEIDRLQNGRCLEAQYSMLATWRRTPRREATLELL 60
QY 57 YAALERMGLDGCVEDL 72
DB 61 GRVLDMDLGLGLEDI 76
RESULT 11

APPLICANT: Ni, Jian
Yu, Guo-Liang
Fan, Ping
Gentz, Reiner
TITLE OF INVENTION: Human
Tumor Necrosis Factor Receptor TR9

RESULT 15
US-10-041-574-23
; Sequence 23, Application US/10041574
; Publication No. US20020168359A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF37591
; CURRENT APPLICATION NUMBER: US/10/041,574
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/527,236
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14

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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-041-574-23

Query Match      33.1%; Score 136.5; DB 4; Length 68;
Best Local Similarity 46.3%; Pred. No. 8.3e-09;
Matches 31; Conservative 12; Mismatches 21; Indels 3; Gaps 2;

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Db      1 RWKEFVRLGLSDHEIDRLQNGRCLEAQSMLATWRRRTREATLELLGRVLRDMDL 60
      |||||  |||  : ||: : ||: |||  |||  |||  : ||: |||  |||

Qy      66 DGCVEDL 72
      |||  |||
Db      61 LGCLEDI 67
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Search completed: March 20, 2006, 08:05:09
Job time : 44 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions **.rnpm** and **.rnpn**

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions **.rapm** and **.rapn**

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

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